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USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-628-380-8
                                                                                US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 4
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                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:

APPLICANT: YONG MING LI
APPLICANT: HILLS VIASSAMA
APPLICANT: HILLS VIASSAMA
TITLE OF INVENTION: RADPRODUCTS, AND METHODS OF THEIR USE
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCES:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackenback Avenue
CITY: Hackenback
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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                                                                              94.3%; Score 66; DB 1; Length 18; 100.0%; Pred. No. 3.3e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION 1436
PRIOR APPLICATION BATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: JUNE 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson E8Q., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1870-5800
TELECOMMUNICATION 1870-7800
TELECOMMUNICATION 2013
SEQUENCE CHARACTERISTICS:
LINGTH 18 AMINICA 2013
                                                                                                                                                                                                                                                                                                                      RESULT 2
US-08-485-948-8
Sequence 8, Application US/08485948
; Patent No. 5855882
; OTHER INFORMATION: (20-37)"
US-08-204-487-3
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DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 100.
Matches 11; Conservative
                                                                              Ouery Match
Best Local Similarity 100.0
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
                                                                                                                                                                                          1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                        1 CFOWORNMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-485-948-8
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1 CFQWORNMRKV 11

CFOWORNMRKV 11

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Sequence 8, Application US/08628380

Patent No. 5891341

GENERAL INFORMATION:
APPLICANT: LI, YONG MING
APPLICANT: CERAMI, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERANA
APPLICANT: ANTHONY CERANA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDFRODUCTS, AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
94.3%; Score 66; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 3.3e-05;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER FALTABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION UNMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              947-1-008 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1
FELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-475-055-8; Sequence 8, Application US/08475055; Patent No. 596245; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      411 Hackensack Avenue
                                                                                                                                                                                                                                              Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 amino acida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                 CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQRNMRKV 11
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us-09-743-107b-79.rai

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TISSUE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
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Sequence 3, Application US/07755161A

Fatent NO. 5304631

GENERAL INFORMATION:

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: Weshington

CONT. Washington
                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FOC COMPATIBLE
COMPUTER: IBM FOC COMPATIBLE
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/475,055
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 66; DB 2; Le
Pred. No. 3.3e-05;
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100.0%; Pred. No. ...
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MEDIUM TYPE: Diakette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/ACENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                Hackensack
: New Jersey
RY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQRNMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
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; FRAGMENT TYPE:
US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                          07601
                                                  CITY: Hac
STATE: Ne
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "thiol group of
Cys residue at location 2 connected by disulfide bond with
thiol group of Cys residue at location 19"
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER:
FILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. CHECK JT.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: 33,367
TELECHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITS:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: /note=
OTHER INFORMATION: thiol g
FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
ILBUGTH: 20 amino acids
ITYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHROMOSOME/SEGMENT: MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
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94.3%; Score 66; DB 1; Length 20;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: YAMAWOTO, NAOKI
APPLICANT: YAMAWOTO, NAOKI
APPLICANT: NAKASHAM, HIDEKI
APPLICANT: NAKASHAM, HIDEKI
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: DOSAKO, SHIN'ICHI
APPLICANT: CAWASAKI, YOSHIHRO
APPLICANT: CHIDA, TOSHIAKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: NHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY AGENT IRPORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
RECIPERENCE TOOKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08204487
Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: THIBEAULT: 53 STATE STREET BOSTON
                                                                                                           NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 11; Conservative
            IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: MA
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
CITY: BC
                                                                                                                                                                                                                                                                                            JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-204-487-1
                                                                                                                                                                                                                                                     AUTHORS:
                                                                                                                                                                                                                                                                                                               VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                      PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
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                    Indela
                                                                                                                                                                                       Sequence 3, Application US/07891174;
Patent No. 5317084;
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
Pred. No. 3.7e-05;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAX-1992
CLASSIPECATION 530
PR.OR APPLICATION 530
PR.OR APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER: 33,367
TELECHONE: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
  Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE
                                                       1 CFOWORNMRKV 11
                                                                                          2 CFOWORNMRKV 12
                                                                                                                                                                                                                                                                                                                                                                                                                STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAP POSITION:
UNITS:
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CELL LINE:
ORGANELLE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LIBRARY:
                                                                                                                                                      RESULT 6
US-07-891-174-3
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OTHER INFORMATION: //ote= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" PUBLICATION INFORMATION:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
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us-09-743-107b-79.rai

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ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGIESTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELEPCOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                              Matches 11; Conservative
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MOLECULE TYPE: peptide
                                                                                                                   1 CFQWQRNMRKV 11
                                                                                                                                             2 CFQWQRNMRKV 12
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                                       Query Match
Best Local Similarity
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US-08-381-984-24
    US-08-256-771-24
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Patent No. 565691
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                        ;
0
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100.0%; Pred. No. 3.7e-05;
ive 0; Mismatches 0; Indels
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cyg regidues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                   /note= "ANTIBACTERIAL PEPTIDE DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 2005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARR: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIPICATION 514
PRICR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                           LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                    Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
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MOLECULE TYPE: peptide
                                                                                                  single
                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                      CTHER INFORMATION: D. CURS. O'CHER INFORMATION: D. US-08-204-487-1
                                                                                                                                                                              NAME/KEY: Peptide
                                                                            TYPE: amino acid STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                2 CFOWORNMRKV 12
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20005
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STATE: D.C.
COUNTRY: U.
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US-08-256-71.25

US-08-256-71.25

Sequence 25, Application US/08256771

Patent No. 5656591

GENERAL INFORMATION:
PAPELICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:
ADDRESSEE: Menderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Mashington
STATE: D.C.
STATE: D.C.
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| OTHER INFORMATION: /note= "Cys residues are protected to
| OTHER INFORMATION: prevent disulfide bond"
| US-08-256-771-25
94.3%; Score 66; DB 1; Length 20; 100.0%; Pred. No. 3.7e-05; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 94.3%; Score 66; DB 1; Length 20; Best Local Similarity 100.0%; Pred. No. 3.7e-05; Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: UJY 22, 1994
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER:
PRIOR APPLICATION NUMBER:
FILING DATE:
RILING DATE:
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Sequence 4, Application US/09508734

GENERAL INFORMATION:

APPLICATIN: Sawyang Genex Corporation

TITLE OF INVENTION: Waseful microorganism thereof

TITLE OF INVENTION: Waseful microorganism thereof

TITLE OF INVENTION: UNMBER: US/09/508,734

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1998-07-13

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "cysteine residues at positions 2 orner information: /note= "cysteine residues at positions 2 orner information: and 19 are chemically modified to prevent disulfide linkage" US-08-381-984-25
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                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
            805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25:
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Best Local Similarity 100.
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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STREET: 805
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STRANDEDNESS: sin
                                                                                U.S.A.
                                                                                                       20002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                   COUNTRY:
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OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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94.3%; Score 66; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 3.7e-05;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                           ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25, Application US/08381984
Fatent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
PILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
               Sequence 24, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
NIAME: WALKEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                      20002
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US-08-381-984-25
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LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94.3%; Score 66; DB 1; Length 25; 100.0%; Pred. No. 4.6e-05; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:

PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: modified site LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 11; Conservative
                                                                                                                                 TELEPHONE: 202-371-885
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNMRKV 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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                                                                                                                                                                                                                                                                                                                                       Sequence 6, Application US/09508734

Fatent No. 6423509

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION: useful microorganism thereof

CURRENT PRING DATE: 2000-06-01

FRICE REPERENCE: PA/SYG/00139

CURRENT PRING DATE: 1999-07-14/KR99/00373

FRICE RILING DATE: 1999-07-14/FR99/00373

FRICE RILING DATE: 1999-07-13

FRICE RILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 12

SSOFTWARE: Kopatentin 1.71

SSOFTWARE: Application Visit No. 6

LENGTH: 24
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                                                                                                        94.3%; Score 66; DB 4; Length 22; 100.0%; Pred. No. 4e-05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     94.3%; Score 66; DB 4; Length 24; 100.0%; Pred. No. 4.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION: ADMINA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 100.
Matches 11; Conservative
                                                                                                                              Best Local Similarity 100.
Matches 11; Conservative
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                           1 CFQWQRNMRKV 11
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US-07-755-161A-10
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US-09-508-734-6
                                                                US-09-508-734-4
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                                                                                                          Query Match
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Gaps

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Search completed: February 21, 2003, 07:50:35 Job time : 8.7 secs
                                                                                                                                                                                                                                              DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWORNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CFOWORNMRKV 14
                                                                                                                                     JOURNAL:
                                                                                                                                                           VOLUME:
                                                                                                                                                                                  SSUE:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                              GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent TITLE OF SEQUENCES: 10 CORRESPONDENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: DisplayWite
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
US-07-891-174-10; Sequence 10, Application US/07891174; Patent No. 5317084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acids STRANDEDNESS: single TOPOLGGY: linear MOLECULE TYPE: HYPOTHETICAL: ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified site LOCATION: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-371-8856
TELEX:
                                                                                                                                                                                                                                                                                                                 ZIP: 20005
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY:
CLONE:
POSITION:
CHROMOSOME,SEGMENT:
MAP POSITION:
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HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
ORGANISM:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
PUBLICATION: thiol group of Cys residue at location 4"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 94.3%; Score 66; DB 1; Length 25; Best Local Similarity 100.0%; Pred. No. 4.6e-05; Matches 11; Conservative 0; Mismatches 0; Indels
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us-09-743-107b-79.rapb

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(without alignments)
35.508 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpaa/USOB_NEW PUB.pep:*
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/ cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156504 segs, 31069816 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*
                                                                                                                    - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                    OM protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                             Run on:
                                                                                                                                                                                                                                                                                                     Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Appl Sequence 58, Appl Appl: 47985, Sequence 2, Appl: Sequence 22, 3 Sequence 8, Ap Sequence 29, 3 Sequence 30, Sequence 23, Sequence 20, Sequence 58, Sequence 58, Sequence 8, Sequence 58, Sequence 6, Sequence 2, Sequence 2 Description Sequence 3 Sequence Sequence Sequence US-09-798-869-2 US-09-798-869-2 US-09-798-869-2 US-09-798-869-3 US-09-798-869-3 US-09-798-869-3 US-09-798-869-4 US-09-798-869-4 US-09-798-869-2 US-09-798-869-2 US-09-798-869-2 US-09-798-869-3 US-09-798-869-3 US-09-798-869-3 US-09-798-869-3 US-09-798-869-3 US-09-798-869-3 US-09-798-869-3 US-09-798-869-3 US-09-798-869-3 US-09-888-320-2 US-10-066-500-58 US-10-002-796-58 US-10-066-273-58 US-10-066-494-58 US-09-904-536-8 SUMMARIES Query Match Length DB Result

9, A 11, 12, 13,	Sequence 13, Appl Sequence 15, Appl Sequence 16, Appl Sequence 17, Appl Sequence 18, Appl	Sequence 10, Appl Sequence 6, Appli Sequence 1, Appli Sequence 6, Appli	Sequence 1, Appli Sequence 119, App Sequence 119, App Sequence 119, App Sequence 119, App	Sequence 119, App Sequence 14, Appl Sequence 6, Appli Sequence 24, Appl	Sequence 30, Appl Sequence 32, Appl Sequence 28, Appl Sequence 10, Appl
10 US-09-904-536-9 10 US-09-904-536-11 10 US-09-904-556-12 10 US-09-904-536-13	10 US-09-004-536-11 10 US-09-904-536-15 10 US-09-904-536-16 10 US-09-904-536-17 10 US-09-904-536-18	10 US-09-904-536-10 9 US-10-095-449-6 10 US-09-448-378-1 10 US-09-983-806-6	10 US-09-904-536-1 9 US-09-978-295A-119 9 US-09-978-697-119 9 US-09-978-192A-119 9 US-09-999-832A-119		10 US-09-981-649A-30 10 US-09-981-649A-32 10 US-09-981-649A-28 9 US-09-881-579-10
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ALIGNMENTS

Sequence 2, Application US/09798869
Fublication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CT/GB99/02851
PRIOR FILING DATE: 1999-08-31
SOFTWARE: FASESEQ FOR WINDOWS VERSION 4.0 ORGANISM: HOMO SAPIENS RESULT 1 US-09-798-869-2 US-09-798-869-2 SEQ ID NO 2 TYPE: PRT

Gaps 0; 94.3%; Score 66; DB 9; Length 15; 100.0%; Pred. No. 3.3e-05; ive 0; Mismatches 0; Indels 11; Conservative Query Match Best Local Similarity Matches 11; Conserv

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CFQWQRNMRKV 11 CFOWORNMRKV 13 à g

Sequence 20, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURDAL
APPLICANT: RALDUR SVEINBA (RNSSON US-09-798-869-20 RESULT 2

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Gaps

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94.3%; Score 66; DB 9; Length 694; 100.0%; Pred. No. 0.0012; tive 0; Mismatches 0; Indels

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11; Conservative
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Query Match
Best Local Similarity
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ORGANISM: CAPRINE
                                                                                                                                                                                  9-698-862-60-SD
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LENGTH: 15
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                                Matches
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APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                  DB 9; her.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
           FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT TILING DATE: US/01-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR RILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSSESEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMINICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                  94.3%; Score 66; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.8
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS: ADDRESSE: Jacobson,
   APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                    TYPE: PRT;
CRGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                          3 CFOWORNMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
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APPLICANT: (YSTEIN REKDAL
APPLICANT: HEALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARG VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PELING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSEED FOR WINDOWS Version 4.0
                                                                                                                                                                                                                     APPLICANT: JORGALION SIGGRA SENDESN
APPLICANT: JORGALION SIGGRA
APPLICANT: JEALUN SUGIND SYENDESN
APPLICANT: JEALUN SYEINBU (RNSSON
APPLICANT: LARS UORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 201-02-27
PRIOR PLILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GE998938.4
PRIOR FILING DATE: 1998-08-28
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Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                           Sequence 6, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
22 CFOWORNMRKV 32
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Best Local Similarity
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Matches 10; Conserv
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Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGHED SVENDSEN
APPLICANT: RALDUR SVETING (RNSSON
APPLICANT: BALDUR SVETING (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
                                                                                                                                     Sequence 4, Application US/09798869 Publication No. US20030022821Al GENERAL INFORMATION:
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Matches 7; Conservative
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1 CFQWQRNMRKV 11
                                    3 CYQWQWRMRKL 13
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Matches 7; Conserv
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ORGANISM: MURINE
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US-09-798-869-22
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Pred. No. 0.0054;
2: Mismatches 1; Indels
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  Indels
  1,
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APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEIRBJ (RNSSON
APPLICANT: LARS VORLAND
ITTLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASESEQ for Windows Version 4.0
SSOFTWARE: FASESEQ for Windows Version 4.0
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Publication No. US20030022821A1

GENERAL INFORMATION:

APPLICANT: GYSTEIN REKDAL

APPLICANT: HALDUR SVENDSEN

APPLICANT: BALDUR SVENDSEN

APPLICANT: BALDUR SVENDSEN

APPLICANT: BALDUR SVENDSEN

TITLE OF INVENTION: BIOACTIVE PEPTIDES

TITLE OF INVENTION: BIOACTIVE PEPTIDES

TITLE OF INVENTION: BIOACTIVE PEPTIDES

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: GE9991038.4

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FASTSED for Windows Version 4.0

SEQ ID NO 7

LENGTH: 15
2; Mismatches
                                                                                                                                                                                Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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8; Conservative
                                        1 CFQWQRNMRKV 11
                                                                               CYQWQRRMRKL 13
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Best Local Similarity
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ORGANISM: CAPRINE
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US-09-798-869-23
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  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
GENERAL INFORMATION:
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CTJCB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR PLILING DATE: 1999-08-31
PRIOR PLILING DATE: 1999-08-31
PRIOR PLILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 4
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CURRENT APPLICATION NUMBER: U5/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PELICATION NUMBER: PCT/GB99/02851
PRIOR PELING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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GENERAL INFORMATION:

APPLICANT: DeBarber, Andrea E.

APPLICANT: DeBarber, Andrea E.

APPLICANT: DeBarber, Andrea E.

APPLICANT: DeBarber, Linda-Gail

APPLICANT: The Government of the United States of America

APPLICANT: as represented by The Secretary of the

APPLICANT: Department of Health and Human Services

TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis

TITLE OF INVENTION WIMBER: US/09/888,320

CURRENT APPLICATION NUMBER: US 60/214,187

PRIOR PELICATION NUMBER: US 60/214,187

PRIOR FILING DATE: 2000-06-26

NUMBER OF SEQ ID NOS: 16

SEQ ID NO 2

LENGTH: 489
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) OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.3%; Score 38; DB 9; Length 489; 54.5%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60.0%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.34; tive 3; Mismatches 2; Indels
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                                                              APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVELNBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CDT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1996-08-31
PRIOR PILING DATE: 1996-08-31
PRIOR PILING DATE: 1996-08-31
PRIOR FILING DATE: 1996-08-36
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-864-761-47985
Sequence 47985, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
Sequence 30, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/09888320
; Publication No. US20030013090Al
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 54.5°
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-798-869-30
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US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.34; 2; Indels live 3; Mismatches 2; Indels
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Pred. No. 0.34;
1; Mismatches 3; Indels
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APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-00-227
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
                                                                                                                    APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYBINBJ(RNSSON
APPLICANT: BALDUR SYBINBJ(RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CTJ/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 29, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                 Sequence 8, Application US/09798869; Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 54.50,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQRNMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-798-869-29
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       RESULT 10
US-09-798-869-8
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RESULT 11

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Gaps

FEATURE:

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Gaps

RESULT 12 US-09-798-869-30

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME TITLE REPERBRICE: 93130R1C7
CURRENT APPLICATION NUMBER: US/10/066,500
CURRENT FILING DATE: 2002-02-01
PRIOR APPLICATION NUMBER: 10/002,796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILLING
PRIOR APPLICATION NUMBER.
PRIOR PILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R FILING DATE: 1997-12-16
R APPLICATION NUMBER: 60/074086
R FILING DATE: 1998-02-09
R PILING DATE: 1998-02-09
R FILING DATE: 1998-02-09
R APPLICATION NUMBER: 60/079294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/059588
FILING DATE: 1997-09-17
APPLICATION NUMBER: 60/062285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 60/062816
FILING DATE: 1997-10-24
APPLICATION NUMBER: 60/063082
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FILING DATE: 1997-11-25
APPLICATION NUMBER: 60/069694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/063329
FILING DATE: 1997-10-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/066364
                                                                                                                                                                                                                                                                                                                                                                                                                      Nicholas F. Paoni
Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
Avi J. Ashkenazi
Kevin P. Baker
David A. Botstein
                                                                                                                                                                                                                         Mary E. Gerritsen
Audrey Goddard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colin K. Watanabe
P.Mickey Williams
William I. Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1998-03-25
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                                                                                                                             Napoleone Ferrara
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                                                                                                                                                                                                                                                                       Paul J. Godowski
Austin L. Gurney
                                                                                                                                                                                                                                                                                                                       Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
                                                                                                                                                                             Wei-Qiang Gao
Hanspeter Gerber
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                                                                               Luc Desnoyers
                                                                                                 Dan L. Eaton
                                                                                                                                                    Sherman Fong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zemin Zang
                                                                                                                                                                                                                                                                                                                                                                                                  James Pan
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                                                               APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ·
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OTHER INPORMATION: MAP TO AL096701.14
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EST_HUMAN HIT: AM294800.1, EVALUE 1.00e-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.9%; Score 37; DB 10; Length 21; 83.3%; Pred. No. 3.2; 1.1 Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47985
LENGTH: 21
                                                                                                                               THILE DEPERBREE, ACCOUNTING
THE REPERBREE ACCOUNTING
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR PELICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR FILING DATE: 2000-02-06
PRIOR FILING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-03
PRIOR PLING DATE: 2000-06-04
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2000-09-03
PRIOR PLING DATE: 2001-01-04
PRIOR PLING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-06-30 APPLICATION NUMBER: US 09/774,203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-01-29
                    Rank, David R.
Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFOWRR 21
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FILING DATE: 1998-08-18
APPLICATION NUMBER: 60/099601
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099803
APPLICATION NUMBER: 60/099811

RESULT 15
US-10-066-500-58
Sequence 58, Application US/10066500
Patent No. US20020177165A1
GENERAL INFORMATION:

DB 9; Length 747; 91; PRIOR FILING DATE: 2000-04-03
PRIOR FILING DATE: 2000-04-13
PRIOR APPLICATION NUMBER: 09/664610
PRIOR APPLICATION NUMBER: 09/664610
PRIOR PILING DATE: 2000-09-18
PRIOR PILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: 09/767609
PRIOR APPLICATION NUMBER: 09/767609
PRIOR PILING DATE: 2000-01-08
PRIOR APPLICATION NUMBER: 09/767609
PRIOR PILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: 09/866028
PRIOR PILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: 09/866028
PRIOR APPLICATION NUMBER: 09/866028
PRIOR PILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 09/866028
PRIOR APPLICATION NUMBER: 09/8619330
PRIOR APPLICATION NUMBER: 09/8619330
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR APPLICATION NUMBER: PCT/US99/25109
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PRIOR PLIING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/2109
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PRIOR PLING DATE: 1999-09-01
PRIOR PLING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/2109
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PRIOR PLING DATE: 1999-09-01
PRIOR APPLICATION NUMBER: PCT/US99/2109
PRIOR PLING DATE: 1999-09-01
PRIOR DA

3; Indels 3; Mismatches Query Match 52.9%; Score 37; Best Local Similarity 45.5%; Pred. No. Matches 5; Conservative 3; Mismatci 1 CFOWORNMRKV 11

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Gaps

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Search completed: February 21, 2003, 08:08:07 Job time : 11.55 secs

FILING DATE: 1999-11-10 APPLICATION NUMBER: 09/423844 FILING DATE: 1999-11-12

FILING DATE: 1999-10-18 APPLICATION NUMBER: 09/423741

FILING DATE: 1999-06-14
APPLICATION NUMBER: 09/380137
FILING DATE: 1999-08-25
APPLICATION NUMBER: 09/380138
FILING DATE: 1999-08-25

PRIOR FILING DATE: 1999-08-25 PRIOR APPLICATION NUMBER: 09/380139

FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/403296 FILING DATE: 1999-10-18

FILING DATE: 1999-10-18
APPLICATION NUMBER: 09/403297

APPLICATION NUMBER: 09/332929 FILING DATE: 1999-06-14 APPLICATION NUMBER: 09/333075

FILING DATE: 1999-06-14 APPLICATION NUMBER: 09/333077 FILING DATE: 1999-06-14

FILING DATE: 1999-04-15 APPLICATION NUMBER: 09/332928 FILING DATE: 1999-06-14

311 CVRWQINSRRI 321

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GenCore version 5.1.3
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OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 9.6 Seconds Run on:

(without alignments)
120.168 Million cell updates/sec

70 1 CFQWQRNMRKVA 12 US-09-743-107B-79 Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Sequence:

283224 segs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

1: pir1:* 2: pir2:* 3: pir3:* 4: pir4:* 73:* PIR Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

SH	Description	lactotransferrin r	lactoferrin - qoat	lactoferrin - shee	lactoferrin precur	dynein beta heavy	hypothetical profe	protein kinase (EC	hypothetical prote	ornithine decarbox	hypothetical prote	26S proteasome SU	hypothetical prote		hypothetical prote		probable cytochron	cytochrome P450 ho	RNA la protein - b	probable oxidoredu	hypothetical prote		En/Spm-like transp	ABC transporter sī	hypothetical prote	GGDEF family prote	WD repeat domain p	conserved hypothet	F1511.22 [imported	outer membrane lip
SUMMAKLES	ID	TFHUL	JC2323	852107	A28438	T08030	AD2346	S42867	AH3147	S52784	T28820	E90094	F90580	T35361	AI2343	C70655	T00510	T00513	Plbvbb	E70848	T29571	AB0858	A84471	875233	T46261	C82361	T48933	AE0040	C96582	210
	DB	¦ ⊣	7	7	Н	7	7	7	N	7	~	N	N	7	7	7	N	7	Н	N	7	7	7	7	N	~	7	~	7	7
	Length	711	708	33	707	4568	298	500	121	435	932	205	282	397	464	489	515	543	996	303	361	511	531	266	570	829	1051	119	124	211
÷	Query Match	94.3	77.1	72.9	64.3	61.4		58.6		55.7		54.3	54.3	54.3	54.3	54.3			54.3	•			52.9	•		52.9	52.9	51.4	51.4	51.4
	Score	99	54	51	45	43	42	41	39	39	39	38	38	38	38	38	38	38	38	37	37	37	37	37	37	37	37	36	36	36
	Result No.	1	7	e	4	ហ	φ	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

vif protein - simi flt3 ligand - huma	hypothetical prote cell cycle arrest	hypothetical sh3-c probable cytochrom	hypothetical prote hypothetical prote	trimethylamine-N-o	phytochrome C - so	hypothetical prote inositol 1,4,5-tri	polymyxin B resist	carcinoembryonic a	hypothetical prote
S07989 I38440	T22597 A39654	T39801 B84514	T17324 C84325	G82168	T14803	T04018 A49873	AG0794	D33876	H70.978
0 0	77	0 0	01 01	9	4 79	01 O1	7	N	0
214 235	306	501 518	558 584	820	1135	1274	85	114	222
51.4	51.4	51.4 51.4	51.4	51.4	51.4	51.4 51.4	50.0	50.0	50.0
36	36 36	36 36	36 36	36	36	36 36	35	35	35
30 31	32 33	34 35	36 37	88 0	v 4.	4 4 2	43	44	45

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В	
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lactotransferrin precursor [validated] - human

C;Species: Homo sapiens (man) C;Date: 31-Mar-1992 #sequence

C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000 C;Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74

R,Cho, Y. submitted to the EMBL Data Library, March 1994

A;Reference number: G06820 A;Accession: G01394

A; Status: preliminary; translated from GB/EMBL/DDBJ A; Wolecule type: mRNA

A; Residues: 1-711 <CHO>

A;Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237 R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucleic Acids Res. 18, 5288, 1990
A;Title: Complete nucleotide sequence of human mammary gland lactoferrin. A;Reference number: S11228; MUID:90384839; PMID:2402455

A; Accession: S11228

A; Molecule type: mRNA

A;Residues: 1-148, T',150-422, C',424-711 <REY>
A;Cross-references: BMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416
R;Terg, C.T.; Liu, Y.; Yang, N:; Walmer, D.; Panella, T.
MAD: Endocrinol. 6, 1369-1381, 1392
A;Title: Differential molecular mechanism of the estrogen action that regulates lactofer: A;Reference number: A45401; MUID:93125571; PMID:1480183

A; Accession: A45401

A; Molecule type: DNA A; Residues: 1-15 <TEN>

A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312
A;Experimental source: placenta
A;Experimental source: placenta
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIP:122202)
B;Powell, M.J.; Ogden, J. J. E.
Nucleic Acids Res. 18, 4013, 1990
A;Title: Nucleotide sequence of human lactoferrin cDNA.
A;Reference number: S10324; MUID:90326549; PMID:2374734

A; Molecule type: mRNA A; Accession: S10324

A;Residues: 3-711 <PON>
A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Blochem. J. 276; 349-355, 1991
A;Title: Expression of cloned human lactoferrin in baby-hamster kidney cells. A;Reference number: S15853; MUID:91264786; PMID:2049066

A, Status: nucleic acid sequence not shown, not compared with conceptual translation A; Accession: S15853

A; Molecule type: mRNA A; Residues: 20-31 <ST1>

A; Accession: S20841

A;Molecule type: protein A;Residues: 20-28,'X',30-31 <ST2>

Length 708;

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Score 54;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             names: lactotransferrin
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63.6%;
                                        77.18;
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R;Liu, Y.; Teng, C.T.
                                                                                                                                                                                                                                                                                                                                                                                                     lactoferrin - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 72.9
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                      8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lactoferrin precursor - mouse N;Alternate names: lactotrans:
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                                     Query Match
Best Local Similarity
Matches 8; Conserv
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A; Residues: 3-707 < PEN>
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A; Residues: 1-15 <LIU>
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C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: UC2323
B;C;Peb-1995 #sequence_revision 0; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus
A;Reference number: UC2323; MUID:94380047; PMID:8093048
A;Accession: UC2223
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: mRNA
A, Residues: 3-701, SWRPVN, cPAN>
A, Experimental source: normal breast tissue
R, Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
BL. J. Blochem. 145, 659-666, 1984
A, Title: Human lactorransferrin: amino acid sequence and structural comparisons with oth
A, Reference number: A31000; MJID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Molecule type: protein
A,Residues: 20-140,142-169,171-203, 'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A,Note: this is the final paper in a series
R,Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Bur. J. Blochem. 241, 303-308, 1996
A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
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F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
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R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of 1
A;Eference number: S07160; MUID:88001031; PMID:3477300
A;Accession: S07160
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C.Superfamily: transferrin; transferrin repeat homology

C.Keywords: duplication; glycoprotein

F.359-696/Domain: transferrin repeat homology <-TRH2>

F.325-300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Residues: 436-487,'A', 489-711 cRAD>
A,Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
R;Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
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                                                                                                                                                                                                                                                                                                                                                            A, Reference number: A61169, MUID:91235214, PMID:1674448
A, Accession: A61169
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C;Superfamily: transferrin; transferrin repeat homology
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Uul-1955 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Bicchim. Biophys. Acta 1434, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a A;Reference number: S52107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A28438; A41205
R;Pentecost, B.T.; Teng, C.T.
Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactoransferrin is the major estrogen inducible protein of mouse uterine secré
A;Reference number: A92596; MUID:87280033; PMID:3611056
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J. Biol. Chem. 26, 21880-21885, 1991
A.Fritle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A.Reference number: A41205, MUID:92042099; PMID:1939212
                            Gaps
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Fi20-707/Product: lactotransferrin #status predicted <MAT>
Fi386-695/Domain: transferrin repeat homology <TRH2>
Fi384-695/Domain: cranbohydrate (Asn) (covalent) #status predicted
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                                1; Indels
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A;Residues: 1-33 <QIA>
C;Superfamily: transferrin; transferrin repeat homology
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C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
0.12;
                            2; Mismatches
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C;Superfamily: ornithine decarboxylase
C;Keywords: carbon-carbon lyase; carboxy-lyase; phosphoprotein; polyamine biosynthesis; ]
                 R;Baur, B.; Winter, K.; Fischer, K.; Dietz, K.
submitted to the EMBL Data Library, March 1994
A;Description: Molecular cloning and characterization of several protein kinases from pl
A;Reference number: S42864
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A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Atu4804 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
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C;Species: 19-may-1995 #sequence_revision 21-Jul-1995 #text_change 08-Sep-2000
C;Accession: S55347; S52784
R;von Besser, H.; Niemann, G.; Domdey, B.; Walter, R.D.
Biochem, J. 308, 635-640, 1995
A;Title: Molecular cloning and characterization of ornithine decarboxylase cDNA of the A;Reference number: S55347; MUID:95290001; PMID:7772052
                                                                                                                                                                                                                 A; Cross-references: EMBL:230330; NID:9457708; PIDN:CAA82991.1; PID:9457709 C; Superfamily: Arabidopsis thaliana protein kinase T518.9; protein kinase homology C; Kywords: ATP; phosphotransferase; protein kinase F:71-379/Domain: protein kinase homology <KIN> F:71-379/Domain: protein kinase ATP-binding motif
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A,Reference number: AB2577; PMID:11743193
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C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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Pred. No. 9.3;
2; Mismatches
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Best Local Similarity 77.55
Best Local 7; Conservative
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Best Local Similarity
                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-500 <BAU>
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A; Residues: 1-435 < VON>
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A;Molecule type: DNA
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C; Accession: S42867
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Anote: Nostoc sp.
Anote: Nostoc sp.
Strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C,Accession: AD2346
F,Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
                                                                                                                                                                                    C,Accession: T08030
R;Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes. A;Reference number: Z16302; WUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium And
A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: IX
A;Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3;
3334/3; 3686/3; 3882/3; 4240/3
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A;Cross-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein kinase (EC 2.7.1.-) - spinach
C;Species: Spinacia oleracea (spinach)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 19-Jul-2002
                                                                                                                                                            C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4568 cMIN.
A;Cross-treferences: EMIL: U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
A;Experimental source: strain 21gr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C,Superfamily: dynein heavy chain, ciliary
C;Keywords: nucleotide binding, P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                                          Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                       dynein beta heavy chain - Chlamydomo
C;Species: Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61.48;
54.58;
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Best Local Similarity 77.0.
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Best Local Similarity
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A,Note: Nostocs sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Datesion: Alaxaya
R;Accession: Alaxaya
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch: Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, É
N, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans
A;Reference number: AB1807; MUID:21595285; PMID:11759840
              hypothetical protein MYPU_5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Species: Mycoplasma pulmonis
C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: F90580
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pull
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Residues: 1-397 <MUR>
A, Cross-references: EMBL:AL079348; PIDN:CAB45460.1; GSPDB:GN00070; SCOEDB:SC6673.04
                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AL445566; PID:g14089965; PIDN:CAC13723.1; GSPDB:GN00153 A;Experimental source: strain UAB CTIP C;Genetics:
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A;Cross-references: GB:BA000019; PIDN:BAB76003.1; PID:g17133440; GSPDB:GN00179
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32;
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Pred. No. 32;
3; Mismatches
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Pred. No. 45;
2; Mismatches
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C;Genetics:
A;Gene: SCOEDB:SC66T3.04
                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.3%;
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es 6; Conserv
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Best Local Similarity
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A; Genetic code: SGC3
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C;Species: nucleomorph Guillardia theta
C;Species: nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: B90094
C;Accession: S: Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: CESP:F07C3.1
A;Map position: 5
A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599
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A;Residues: 1-205 <DOU>
A;Cross-references: GB:AF165818; NID:g13794510; PIDN:AAK39885.1; GSPDB:GN00150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-932 <FAV>
A;Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A;Experimental source: strain Bristol N2; clone F07C3
                                                                                                                                                                                                                                                                                                                                C, Species: Caenorhabditis elegans
C, Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C, Accession: T28820
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                                                                                              Gaps
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F;76/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted
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Pred. No. 70;
                                            DB 2; Length 435; 33;
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                                                                                              2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   R.Favello, A.; Gattung, S. submitted to the BMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F07C3.
A;Reference number: Z20528
                                                                                                                                                                                                                                                                                                         hypothetical protein F07C3.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55.7%; Sco. 70.0%; Pred. No. , v, 70.0%; 1; Mismatches
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                                                                                           1; Mismatches
                                               Score 39;
Pred. No.
                                            55.7%;
70.0%;
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Best Local Similarity 62.5%;
Matches 5; Conservative
                   Ouery Match
Best Local Similarity 70.v.
7, Conservative
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C; Keywords: nucleomorph
                                                                                                                                          3 OWORNMRKVA 12
                                                                                                                                                                                       61 ÓWÓRTMPRVA 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: T28820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: E90094
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Matches

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RESULT 12

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0;

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                                                         Query Match 54.3%; Score 38; DB 2; Length 464; Best Local Similarity 54.5%; Pred. No. 53; Matches 6; Conservative 2; Mismatches 3; Indels
C;Genetics:
A;Gene: all4304
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2 FOWORNMRKVA 12

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Op

probable monooxygenase - Mycobacterium tuberculosis (strain H37RV)
C.Specias: Mycobacterium tuberculosis
C.Specias: Mycobacterium tuberculosis
C.Specias: Mycobacterium tuberculosis
C.Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-oct-1999
C.Accession: C70655
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome A;Reference number: A70500; MUID:9829597; PMID:9634230
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70655
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Roos-references: GB:283864; GB:AL123456; NID:93261687; PIDN:CAB06212.1; PID:e301250; A;Experimental source: strain H37RV
C;Genetics:
A;Genetics:
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A;Genetics:

0; Gaps Query Match 54.3%; Score 38; DB 2; Length 489; Best Local Similarity 54.5%; Pred. No. 56; Matches 6; Conservative 2; Mismatches 3; Indels

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1 CFQWQRNMRKV 11 ò 253 COKWPRRMRKM 263

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Search completed: February 21, 2003, 07:47:51 Job time : 10.65 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 4.6 Seconds
(without alignments)
108.199 Million cell updates/sec Run on:

US-09-743-107B-79 70 1 CFQWQRNMRKVA 12 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P02788 homo sapien	capra		P08071 mus musculu	_					P37143 methylobaci	Q19910 caenorhabdi				P49771 homo sapien	P26448 saccharomyc	008328 bacillus st						P30453 homo sapien	Q9pjj9 chlamydia m				Q39017 arabidopsis		~	POSSER brome mosai	מ דר סוווני
SUMMARIES	ID	TRFL HUMAN	TRFL_CAPHI	TRFL CAMDR	TRFL MOUSE	DYHB CHLRE	TRFL HORSE	DCOR_PANRE	RPOB_LIBAF	V1A BBMV	DHOM METGL	YKYL CABEL	YJ19_SYNY3	LOLB_VIBCH	VIF SIVS4	FL3L HUMAN	BUB2 YEAST	GLGA_BACST	PHYC_SORBI	IP3T HUMAN	PMRD SALTY	IL2A_BOVIN	IL2A_SHEEP	1A34 HUMAN	SYH CHLMU		PDI1 HUMAN	TRFL BUBBU	KDG1_ARATH	YOO8 HUMAN	YNR2 CAEEL	V1 A FMU	
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	Score	99	54	49	45	43	41	39	38	38	37	37	37	36	36	36	36	36	36	36	35	35	35	35	35	35	35	35	35	35	35	7.5	ו
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YE83_METJA RL24_SCHPO	VIF HV2SB VIF HV2ST	Y495 SYNY3	VA16 VACCV VNS2 DSDNV	NLA DROME	NORC CHLTR	CATK RAT	MURG NEIMA	MURG_NEIMB
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3.4	36	38	3 9 9 9	41	42	43	44	45

ALIGNMENTS

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MCCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U. Sagripanti J.L.;
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MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=88001031; PubMed=3477300; Rado T.A., Well X., Benz E.J. Dr.; "Isolation of lactoferrin clonA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
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                                                                                                                                                   MEDLINE-85076667; PubMed-6510420; Mazurier J., Schoentgen F., Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F., Legrand D., Spik G., Montrauli J., Jolles P.; "Human lactotransferrin: amino acid sequence and structural comparisons with other transferrins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 binding properties and crystal structure of the histidine-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        <-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.</pre>
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                                                       Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA.";
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MEDLINE=99190892; Pubmed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 609-711.
MEDLINE=82262043; PubMed=7049727;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 436-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 237-711 FROM N.A.
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                  rissum=Mammary gland;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF AN ANILAY, USOBLELL BLAKESURIES, FUND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOFERROXINS A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
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Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
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-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                          MEDLINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
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                                                                                                         Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- DOMAIN: COMPOSED OF TWO HOMOLOGGUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                             ANGSTROMS).
                                                                                                                                                                                                                                                                               Agric. Biol. Chem. 54:1803-1810(1990).
                                            Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                              CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Secreted.
                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTRC MEDLINE=99192677; PubMed=10089508;
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EMBL; U07643; AAB60324.1; -.
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M83205; AAA58656.1; -.
M18642; AAA86665.1; -.
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1LCT; 31-OCT-93.
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1LGC; 31-AUG-94.
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21-APR-97.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
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HSSP; O77698; 1CE2.
InterPro; IPROUI156; Transferrin.
Pfan; PRO0425; transferrin.
PRINTS; PRO0422; TRANSFERRIN.
SMART; SM00094; TR PER; 2.
PROSITE; PS00206; TRANSFERRIN.1; 2.
PROSITE; PS00206; TRANSFERRIN.2; 2.
PROSITE; PS00206; TRANSFERRIN.2; 2.
PROSITE; PS00207; TRANSFERRIN.3; 2.
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             94.3%; Score 66; DB 1; Length 711; 100.0%; Pred. No. 0.00027; ive 0; Mismatches 0; Indels
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                029477; 029479;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-UNA-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
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                                            11; Conservative
                                                                                                                                                                                      STANDARD;
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                             Local Similarity
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SEQUENCE FROM N.A.
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Paramasivam M., Srintvasan A., Singh R., Sahani M.S., Singh T.P.;
Paramasivam M., Srintvasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (UN-1999) to the EMBL/GenBank/DDBJ databases
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUBMILY BICARRONATE (BY SIMILARITY).
-!- SUBGILLULAR LOCATION: Secreted.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Somall; TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
int. Dairy J. 9:481-486(1999)
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Q -> K (IN REF. 2).
F -> P (IN REF. 2).
F -> P (IN REF. 2).
S -> R (IN REF. 2).
P -> R (IN REF. 2).
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Lactotransferrin precursor (Lactoferrin).
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
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77358 MW;
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BKNBL; AJ131674; AAF82241.1; -.
BKNBL; AF165879; AAF82241.1; -.
BKSP; O77811; 1BIX.
INTESPC; IPRO01156; Transferrin.
PFINITS; PRO0425; TRANSFERRIN.
SWART; SMO0094; TR FEX; 2.
PROSTIE; PSO0206; TRANSFERRIN. 1; 2.
PROSTIE; PSO0206; TRANSFERRIN. 2; 2.
PROSTIE; PSO0206; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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G -> A (IN REF. 2).
LLS -> PLF (IN REF. 2).
L -> F (IN REF. 2).
A -> PLF (IN REF. 2).
A -> P (IN REF. 2).
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BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu Y., Teng C.T., "Characterization of estrogen-responsive mouse lactoferrin promoter."; "Characterization of estrogen-responsive mouse lactoferrin promoter."; J. Biol. Chem. 266:21880: ARE IRON BINDING TRANSPORT PROTEINS WHICH -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIJINE-87280033; PubMed-3611056;
Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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-:- SUBCELLULAR LOCATION: Secreted.
-:- DOMALIN: COMPOSED OF TWO HOMOLOGOUS DOMALINS.
-:- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN.
1.
TRFL MOUSE STANDARD; PRT; 707 AA. P08071; P70590; Q61799; Q922P2; 01-AUG-1988 (Rel. 08, Created) 15-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987).
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SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprot
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J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
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SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydomonas reinhardtii.
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
MR -> IQG (IN REF. 1).
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M -> L (IN REF. 2).

A -> D (IN REF. 1).

A -> D (IN REF. 1).

L -> G (IN REF. 1).

L -> V (IN REF. 1).

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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
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BY SIMILARITY.
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MEDLINE=94274778; Pubmed=8006077;
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ses 7; Conservative
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707 AA;
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-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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InterPro, IPR004273; Dynein_heavy.
Pfam, PF03028; Dynein_heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.
DOMAIN 277 293 COILED COIL (POTENTIAL).
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-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    519961 MW; 9A9A5393C7C36AE7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.; "CDNA sequence of mare lactoferrin."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
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MICROTUBULE-BINDING (POTE
COLLED COLL (POTENTIAL).
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ATP (POTENTIAL).
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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
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COILED COIL (POTENTIAL)
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-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- DIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Pred. No.
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54.5%;
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Best Local Similarity
6; Conserve
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                                                                                                DR InterPro; IPR001156; Transferrin.
DR PEIM; PR004025; Transferrin.
DR SMART; PR00422; TRANSFERRIN.
DR SMART; SM00094; TR PER; 2.
DR PROSITE; PS00205; TRANSFERRIN 1; 2.
DR PROSITE; PS00207; TRANSFERRIN 2; 2.
OR Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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T SIGNAL <1
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                                                                                                                                                                                                                                                                                                                                                                           CDNA of the nematode Panagrellus redivivus.";

Biochem. J. 308:635-640(1995).

-I. CARALYNIC ACTIVITY: L-orithine = putrescine + CO(2).

-I. CORACTOR: PYRIDOXAL PHOSPHATE.

-I. PATHWAY: FIRST STEP AND ALSO THE RATE-LIMITING STEP IN THE PATHWAY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: HOMODINER.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE DECARBOXYLASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001183; Decarbxylse2.

Pfam; PF00278; Orn_DAP_Arg_deC; 1.

Pfam; PF002784; Orn_Arg_deC_N; 1.

PRINTS; PR01179; ODADCREXLASE.

PROSITE; PS00878; ODR_DC_2 1; 1.

PROSITE; PS00879; ODR_DC_2 2; 1.

PROSITE: PS00879; ODR_DC_2 2; 1.

PS00879
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01-NOV-1995 (Rel. 32, Last sequence update)
01-NOV-1995 (Rel. 40, Last amnotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                   MEDLINE=95290001; PubMed=7772052; von Besser H., Niemann G., Domdey B., Walter R.D.; "Molecular cloning and characterization of ornithine decarboxylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Nelspruit;
Planet P., Jagoueix S., Bove J.M., Garnier M.;
"Detection and characterization of the African Citrus Greening
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Pred. No. 11;
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                                                                                                                                        Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida,
Panagrolaimoidea, Panagrolaimidae, Panagrellus
01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-1996 (Rel. 34, Last annotation update) Ornithine decarboxylase (EC 4.1.1.17) (ODC).
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1; Mismatches
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                                                                                                                      Panagrellus redivivus.
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SEQUENCE FROM N.A.
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P41187;
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SEQUENCE
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EMBL; M65138; AAA42740.1; -.
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                                                                                                                                                                                                                                                                         RESULT 10
  SO THE SO THE SO
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                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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             rpoBC operon.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dzianott A.M., Bujarski J.J., "The nucleotide sequence and genome organization of the RNA-1 segment in two bromoviruses: broad bean mottle virus and compea chlorotic
Liberobacter by amplification, cloning and sequencing of the rplKAJL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                              SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                   CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                      SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VITOLOGY 185:553-562(1991).
-1- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFEBASE DOMAIN.
METHYLTRANSFEBASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
                                                                                                                                                                                                                                                                                                                                                                                                                   54.3%; Score 38; DB 1; Length 146; 60.0%; Pred. No. 5.4;
                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                          NON TER 146 146
SEQUENCE 146 AA, 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-001-1993 (Rel. 26, Created)
01-001-1993 (Rel. 26, Last sequence update)
16-007-2001 (Rel. 40, Last annotation update)
1A protein [Includes: Helicase; Methyltransferase].
Broad bean mottle virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 5.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 966 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92074218; PubMed=1962437;
                                                                                                                                                                                                                                                                                                 EMBL; U09675; AAA19557.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWORNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 CVOWSRGARK 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=12301;
                                                                                                                                          BETA' CHAIN.
                                                                      SUBSTRATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mottle virus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Bawden
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bromovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V1A BBMV
Q00020;
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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Pfam; PF03447; NAD binding_3; 1.
PROSITE; PS01042; HOMOSER_DHGENASE; FALSE_NEG.
Oxidoreductase; NADP; Threonine biosynthesis; Isoleucine biosynthesis;
Methionine biosynthesis.

    semialdehyde + NAD(P)H.
    PATHWAY: THIRD STEP IN CONVERSION OF L-ASPARTATE TO HOMOSERINE.
    HOMOSERINE PARTICIPATES IN THE BIOSYNTHESIS OF THREONINE AND THEN ISOLEDCINE AND IN THE BIOSYNTHESIS OF METHIONINE.
    SIMILARITY: BELONGS TO THE HOMOSERINE DEHYDROGENASE FAMILY.

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                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=ATCC 21276;

MOLDINE-B4161493; PubMed=8117070;

MOLOyama H., Maki K., Anazawa H., Ishino S., Teshiba S.;

MOLOyama H., Maki K., Anazawa H., Ishino S., Teshiba S.;

"Cloning and nucleotide sequences of the homoserine dehydrogenase genes (hom) and the threonine synthase genes (thrC) of the Grammagative obligate methylotroph Methylobacillus glycogenes.";

Appl. Environ. Microbiol. 60:111-119(1994).

-I. CATALYTIC ACTIVITY: L-homoserine + NAD(P) (+) = L-aspartate 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methylobacillus glycogenes.
Bacteria; Proteobacteria; beta subdivision; Methylophilus group;
                                                                                                                                                                                                                                                                                                                                                               4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                            54.3%; Score 38; DB 1; Length 966; 50.0%; Pred. No. 37;
                                                                                                                                                                                                                                                                                                                                                        3; Indels
PIR; A41699; PIBVBB.
InterPro: IPR002588; Varal_helicase1.
InterPro: JR8000606; Viral_helicase1.
Pfam; PF01443; Viral_helicase1; 1.
Pfam; PF01660; Vmethyltransf; 1.
Helicase; ATP-binding; Transferase; Methyltransferase.
NP_BIND
SEQUENCE 966 AA; 109621 MW; DF592681D7231C8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  435 AA; 48226 MW; 58468B0E7A81ACAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1994 (Rel. 30, Last sequence update) 30-MAY-2000 (Rel. 39, Last annotation update) Homoserine dehydrogenase (EC 1.1.1.3) (HDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NADP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1994 (Rel. 30, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D14070; BAA40414.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 CFKENKDWTENMRSVA 362
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQ----WORNMRKVA 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
6; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methylobacillus.
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Chaperone; Outer membrane; Lipoprotein; Transport; Protein transport;
-!- SIMILARITY: BELONGS TO THE ABC1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE004289; AAF95326.1; -.
                                                                                                                                                                                                                                  52,9%;
61.5%;
                                                                                                                              EMBL; D90903; BAA17147.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR004565; LolB.
Pfam; PF03550; LolB; 1.
                                                                                                                                                                                                                                                            8; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                              469 FOWORLENMLSIA 481
                                                                                                                                                                                                                                                                                    2 FOWOR--NMRKVA 12
                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR VC2181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                            LOLB VIBCH
ID LOLB VIBCH
AC P57070;
                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cholerae
                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                     RESULT 13
                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation — the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIATE=97061201; PubMed=8905231; MEDIATE=97061201; PubMed=8905231; MEDIATE=97061201; PubMed=8905231; MEDIATE=97061201; Mither Stools, Kotani H., Tanaka A., Asamoto E., Kimura T., Mityajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T., Hosouchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A., "Sequence analysis of the genome of the unicellular cyanobacterium synechocyptis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.9%; Score 37; DB 1; Length 455; 50.0%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                 Miller N., Bradshaw H.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                              Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; U42437; AAA83493.2; -.
Wormbep; F3085.4; CE28552.
Hypothetical protein.
SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synechocystis sp. (strain PCC 6803).
Bacteria, Cyanobacteria, Chroococcales, Synechocystis.
                                                                               16-0cT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein F30B5.4 in chromosome IV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                  Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein slr1919.
SLR1919.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                 STANDARD;
                                                                                                                                                      Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102 CIOWELNER 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNMRK 10
  111 WORDFRRVA 119
                                                                                                                                                                                                                                  STRAIN-Bristol N2;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1148;
                                                                                                                                                                                             NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .,
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                                                                 CAEEL
                                                                                                                                                                                                                                                                                       REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P73121;
                                                                          019910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
YJ19_SYNY3
                                       RESULT 11
YKYL CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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STRAIN=EI TOR NISSE1 / Serctype 01;
MEDLINE=2040683; PubMed=10952301;
Heidelberg U.F., Blene U.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.A.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE LOLA PROTEIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NATURE 406:477-483 (2000).
-!- FUNCTION: PLAYS A CRITICAL ROLE IN THE INCORPORATION OF
LIPOPROTEINS IN THE OUTER MEMBRANE AFTER THEY ARE RELEASED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37; DB 1; Length 566; Pred. No. 33; 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF03109; ABC1; 1.
PROSTIE; PSS0011; PROTEIN KINASE DOM; UNKNOWN 1.
Hypothetical protein; Complete proteome.
SEQUENCE 566 AA; 65078 MW; 0CS0CC04509FDCB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Outer-membrane lipoprotein lolB precursor
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR004147; ABC1.
InterPro; IPR000719; Euk pkinase.
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us-09-743-107b-79.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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      HILLITITITITITITITI BEENER BEENER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "An African primate lentivirus (SIVsm) closely related to HIV-2.", Nature 339:389-392(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
11-0TM-2002 (Rel. 41, Last annotation update)
SL cytokine precursor (Fms-related tyrosine kinase 3 ligand) (Flt3 ligand) (Flt3.
                                   OUTER-MEMBRANE LIPOPROTEIN LOLB.
N-ACYL DIGLYCERIDE (BY SIMILARITY).
FIEF70858484177E CRC64;
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                                                                                                                      DB 1; Length 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89262053; PubMed=2786147;
Hirsch V.M., Olmstead R.A., Murphey-Corb M., Purcell R.H.,
                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25140 MW; 9BCE884EC454BF3D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                 01-0CT-1989 (Rel. 12, Created)
01-0CT-1989 (Rel. 12, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
Virion infectivity factor (SOR protein) (Q protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses, Retroid viruses, Retroviridae, Lentivirus.
                                                                                                                                                                                                                                                                                                                                                 214 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   235 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adduce 333:303-332 (1303).
-!- FUNCTION: DETERMINES VIRUS INFECTIVITY.
                                                                                                                                                              5; Mismatches
                     BY SIMILARITY
                                                                                                                      Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro, IPR000475; Viral_infect. Pfam; PF00559; Vif; 1. PRINTS; PR00349; VIRIONINFFCT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000063; Viral_infect; 1.
                                                           27 N
24379 MW;
                                                                                                                      51.4%;
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Signal; Complete protecme.
                                                                                                                                       Best Local Similarity 45.5
Matches 5; Conservative
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HIV; X14307; VIF$SMMH4.
                                                                                                                                                                                                    2 FOWORNMRKVA 12
                                                                              211 AA;
                                                                                                                                                                                                                                          71 FÓWOKSPOKLS 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               214 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11737;
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                                                                                                                                                                                                                                                                                                                                             SIVS4
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- ALTENATIVE PRODUCTS: 2 isoforms; a 1/membrane-bound (shown here)
and 2/soluble; are produced by alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of human and murine flt3 ligand genomic loci."; Oncogene 11:1165-1172(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=94235842; PubMed=8180375; Lyman S.D., James L., Johnson L., Brasel K., de Vries P., Escobar S.S., Downey H., Splett R.R., Beckmann M.P., McKenna H.J.; "Cloning of the human homologue of the murine flt3 ligand: a growth Eactor for early hematopoietic progenitor cells."; Blood 83:2795-2801(1994).
                                                                                                                                                          MEDLINE=94195428; PubMed=8145851; Maclanahan T., Zurawski S., Hannum C., Culpepper J., Campbell D., McClanahan T., Zurawski S., Bazan J.F., Kastelein R., Hudak S., Wagner J., Mattson J., Luh J., Duda G., Martina N., Peterson D., Menon S., Shanafelt A., Muench M., Kelner G., Namikawa R., Rennick D., Roncarolo M.G., Zlotnik A., Rosnet O., Dubreuil P., Birnbaum D., Lee F.; "Ligand for FLT3/FKZ receptor tyrosine kinase regulates growth of haematopoietic stem cells and is encoded by variant RNAS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=20343011; PubMed=10881197;
Savvides S.M., Boone T., Karplus P.A.;
"Flt3 ligand structure and unexpected commonalities of helical bundles and cystine knots ";
Nat. Struct. Biol. 7:486-491(2000).
-:- FUNCTION: STIMULATES THE PROLIFERATION OF BARLY HEMATOPOLETIC
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: Homodimer (isoform 2).
-!- SUBCELLULAR LOCATION: Type I membrane protein (isoform 1);
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SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE=96032581; PubMed=7566977;
Lyman S.D., Stocking K., Davison B., Fletcher F., Johnson L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SL CYTOKINE. EXTRACELLULAR (POTENTIAL)
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EMBL; U29874; AAA90949.1; -.
EMBL; U29874; AAA90950.1; -.
PDB; 1ETE; 09-UN-00.
Genew; HGNC:3766; FLT3LG.
MIM; 600007; -.
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                                                                                                NCBI_TaxID=9606;
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FT CARBOHYD 126 126 N-LINKED (GLCNAC. ..) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. ..) (POTENTIAL).
FT VARSPLIC 161 178 DSSTLPPPWSPREATA -> VETVFHRVSQDGLDLITS
FT CONFLICT 72 (IN ISOFORM 2).
FT CONFLICT 72 G -> A (IN REF. I).
SQ SEQUENCE 235 AA, 26416 MM, 73895BF693B4CECF CRC64,

Query Match
Best Local Similarity 50.0%; Pred. No. 20,
Matches 5, Conservative 1; Mismatches 4; Indels 0, Gaps 0,
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Search completed: February 21, 2003, 07:27:54 Job time : 5.6 secs

1 CFQWQRNMRK 10 | | | | | | 204 CLHWQRTRRR 213

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Ogucys homo sapien
Ogyrs aries
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GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Q9TR80
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**p bacteria:*

**p fungi:*

**p human:*

**p invertebrate:*

**p mammal:*

**p mhc:*

**p organelle:*

**p phage:*
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sp_bacteriap:*
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01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-DEC-2001 (TrEMBLrel. 19,
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Best Local Similarity
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     [1]
SEQUENCE FROM N.A.
MEDLINE-21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Kaneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Watshida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
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 Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                      Score 57; DB 4; Length 38;
Pred. No. 0.0013;
Mismatches 0; Indels
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SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                           InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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Last annotation update)
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                                                                                                                                                              100.0%; Pred. No.
                                                                                                                                                         Score 57;
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Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
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MEDLINE=95127729; Pubmed=7827104;
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                                 SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
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Hypothetical protein Alr4323.
ALR4323.
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Best Local Similarity 100.(
Matches 10; Conservative
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nes 7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    Mammalia, Butheria, Ceta.
Bovidae, Caprinae, Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWORNMRKV 11
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                                                                                                                                                                                                                    21 FOWORNMRKV 30
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                                                                                                                                                                                                     2 FOWORNMRKV 11
             NCBI_TaxID=9606;
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   Mammalia;
                                                                                                                                 SEQUENCE
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                                                        Sato I.;
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Q8YP77
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MEDILINE-99440505; PubMed=9765386;
Pseguier C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J.,
Puel J., Izopet J.;
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O'Virol. 72:8493-8501(1998).

BMBL; AJ008835; CAA0837.1;
InterPro; IPR000777; GP120.

Pfam; PF00516; GP120:

1.
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SEQUENCE FROM N.A.

PASDLINES-198440505, PubMed=9765386;

PASQLISE C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J.,

Puel J., Izopet J.,
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Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaean sp. strain PCC 7120.";
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Pred. No. 3.8;
                                                                                                                                                                                                         n 60.0%; Score 42; DB 16; Length 298; Similarity 77.8%; Pred. No. 7.2; 7; Conservative 0; Mismatcher
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109 AA; 12015 MW; EEOCA3E4A0A0D0EB CRC64;
                                                                                                           DNA Res. 8:205-213(2001).

EMB1, AP003596; BAB76022.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 298 AA; 34513 MW; 64036E6B52299A9F CRC64;
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Last annotation update)
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(TrEMBLrel. 10, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus
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3 QWQRNMRKVA 12
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78 QWNRTLRKVA 87
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Q9YIJ2
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Q9YJ17
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MEDLINE=98440505; PubMed=9765386;
MEDLINE=98440505; C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J.,
Puel J., Izopet J.; Expet J.; Molecular evidence for mother-to-child transmission of multiple variants by analysis of RNA and DNA sequences of human
"Molecular evidence for mother-to-child transmission of multiple variants by analysis of RNA and DNA sequences of human immunodeficiency virus.";
J. Virol. 72:8493-8501(1998).
EMBL; AJ008839; CAA08301.1;
PIERPL; AJ008839; CAA08301.1;
Pfam: PF00516; GP120.
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                                                                                                                            Query Match
Best Local Similarity 70.0%; Pred. No. 3.8;
Matches 7; Conservative 1; Mismatches 2; Indels
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                                                                                               109 109
109 AA; 12012 MW; FB18E6E4AB546FB0 CRC64;
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109 AA; 12053 MW; 8217D3EA2DFD4C4B CRC64;
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OSYGBS,
01-MAX-1999 (TIEMBLINE). 10, Created)
01-MAX-1999 (TIEMBLINE). 10, Last sequence update)
01-MAX-1999 (TIEMBLINE). 19, Last annotation update)
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
                                                                                                                                                                                                                                                                                                            Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCB _TaxID=11676;
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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J. Virol. 72:843-8501(1998).
BMBL; AJ008843; CAA08305.1; -.
INTERPRO; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
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Q9YQB8
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MEDLINE-98440505; PubMed=9765386;

MEDLINE-98440505; PubMed=9765386;

A Pasquiar C.J.m., Cayrou C., Blancher A., Berrebi A., Tricoire J.,

Topet J., Izopet J., Izopet J.,

"Molecular evidence for mother-to-child transmission of multiple
T variants by analysis of RNA and DNA sequences of human
immunodeficiency virus type I.";

J. Virol. 72:8493-8501(1998).

R EMBL; AJ008841; CAA08298.1; -.

R EMBL; AJ008835; CAA08298.1; -.

R EMBL; AJ008835; CAA08290.1; -.

R EMBL; AJ008835; CAA08290.1; -.

R EMBL; AJ008836; CAA08302.1; -.

R EMBL; COORDESS COORDES
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MEDLINE=98440505; PubMed=9765386; Pasquier C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J., Pasquier C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J., Puel J., Izopet J.; I
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 Q9YIJZ PRELIMINARY; PRT; 109 AA.
Q9YIJZ;
U-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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01-WAY-1999 (TrEMBLrel. 10, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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L SUDMILLE (MAR. 1994) to the EMBL/GenBank/DDBJ databases.

SIDMILLE (MAR. 1994) to the EMBL/GenBank/DDBJ databases.

-1 - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

R EMBL; 230330; CAA82991.1; -.

R EMBL; 230330; CAA82991.1; -.

R InterPro; IPR000219; Pkinase.

R InterPro; IPR000290; Ser Lhr_pkinase.

R Pfam; PF00069; pkinase; I.

R Pfam; PF00069; pkinase; Z.

R Pfam; PF0001; PR00019; Euk pkinase; Z.

R Pfam; PR0013; Sirk; J.

R PROSITE; S800107; PROTEIN KINASE DOW; 1.

R PROSITE; PS00101; PROTEIN KINASE DOW; 1.

R PROSITE; PS00101; PROTEIN KINASE ST);

R PROSITE; PS00101; PROTEIN KINASE ST);

R PROSITE; PS00108; PROTEIN KINASE ST; 1.

W ATP-Dinding; Kinase; Seriale(Ihreonine-protein kinase; Transferase.)

SEQUENCE 500 AA; 57996 MW; 55798056AC357C07 CRC64;
                                                                                                                               Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
VCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                 Baur B., Winter K., Fischer K., Dietz K.; "Molecular cloning and characterization of several protein kinases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58.6%; Score 41; DB 10; Length 500; 77.8%; Pred. No. 19; 1; Mismatches 1; Indels
                                                           Last sequence update)
Last annotation update)
500 AA.
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                        Created)
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InterPro; IPR000777; GP120.
Pfam; PF00516; GP120; 1.
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                                                                                                                    Spinacia oleracea (Spinach).
                Q41383;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
                                                                              01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 77...
7, Conservative
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae, euasterids I; Lamiales; Pedaliaceae; Sesamum.
                                                                                                                                       MEDLINE=98440505; PubMed=9765386;
Pasquier C.J.M., Cayrou C., Blancher A., Berrebi A., Tricoire J.,
Puel J., Izopet J.;
                                                                                                                                                                                            "Molecular Evidence for mother-to-child transmission of multiple variants by analysis of RNA and DNA sequences of human immunodeficiency virus type 1.",
J. Wirol. 72:8493-8501(1998).

EMBL; AJ009061; CAA08523.1; -.

EMBL; AJ008042; CAA08304.1; -.

Interpro; IPR00077; GP120.

Pfam; PF00516; GP120.;

AIDS; Coat protein; Envelope protein; Glycoprotein.
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1. Agric. Food Chem. 47:4932-4938 (1999).

EMBL; AF091641, AAD42943.1;

InterPro; IPR003612; AAI.

InterPro; IPR0010617; Napin.

InterPro; PR0010617; Napin.

Fram; PF00234; tryp_alpha_amyl inhbtr.

PRINTS; PR00496; NAPIN.

SMART; SM0499; AAI; 1.

SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                    Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
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STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Envelope protein (Fragment).
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Best Local Similarity 66.7
Matches 6; Conservative
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Q9XHP1

RESULT 11 Q9XHP1

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STRAIN=NJS182;

Brandful J.A.M., Ampofo W.K., Janssens W., Adu-Sarkodie Y.,

Brandful J.A.M., Amyofo W.K., Janssens W., Adu-Sarkodie Y.,

Brandful J.S., Yamamoto N.,

Ishikawa K., Sata T., Kurata T.;

"Genetic and phylogenetic analysis of HIV-1 strains from Southern
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9138 MW; 2D43DCD554295572 CRC64;
Last sequence update)
Last annotation update)
                                                                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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RESULT 12 Q41383

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Yatapoxvirus.
NCBL_TaxID=38804;
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Capripoxvirus.
NCBI_TaxID=59509;
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STRAIN=NEETHLING 2490;
MEDLINES-21294945;
MEDLINES-21294945;
FubMed=11435593;
Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"Genome of lumpy skin disease virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tulman E.R., Afonso C.L., Lu Z., Zsak L., Kutish G.F., Rock D.L., Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
BREL, ARZS5281 ARK85069.1; -.
InterPro: IPR04251; DUF230.
Pfam; PF03003; DUF230; 1.
SEQUENCE 377 AA; 43937 MW; FA3B4316DBE28D3B CRC64;
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   57.1%; Score 40; DB 15; Length 81; 60.0%; Pred. No. 4.2; ive 3; Mismatches 1; Indels
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"DNA sequence of Yaba virus BamH1-D fragment.";
Submitted (CCT-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB018404; BAA88879.1; -.
InterPro; IRR004251; DUF230.
Pfam; PF03003; DUF230.
NON_TER 329 329
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                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
YB-D1L protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q91MQ5 PRELIMINARY; PRT; 377 AA.
091MQ5,
01-DEC-2001 (TYEMBLrel. 19, Created)
01-DEC-2001 (TYEMBLrel. 19, Last sequence update)
01-JUN-2002 (TYEMBLrel. 21, Last annotation update)
ESDV108 putative myristylated membrane protein.
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STRAIN=NEETHLING 2490;
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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                    Dolphin GT;
                                                                         Human lactoferrin derived peptide SEQ ID NO:80.
                                                                                                                                                                                                                                                                                                                  Hanson LA, Mattsby-Baltzer I, Baltzer L,
          AAY78080 standard; Peptide; 12 AA
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98SE-0002562.
98SE-0004614.
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                                                   25-APR-2000 (first entry)
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                                                                                                                                                   Homo sapiens.
Synthetic.
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29-DEC-1998;
                                                                                                                                                                                                         13-JAN-2000
                               AAY78080;
AAY78080
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uniary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                      Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial; anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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100.0%; Pred. No. 4.8e-05;
tive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY78071 standard; Peptide; 12 AA.
                                                                    Claim 22; Page 36; 102pp; English.
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98SE-0002562.
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Matches 12; Conservative
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17-JUL-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human

Claim 22; Page 35; 102pp; English.

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                      Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:38.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY78038 standard; Peptide; 12 AA.
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98SE-0004614.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
             Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                                                       Length 12;
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                                                                                                                                                                                     Score 58; DB 21;
Pred. No. 0.00059;
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Synthetic.
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                                                                                                                                                                                                                                                                                                                    Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                          Length 12;
                                                                      1; Indels
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                                        Score 58; DB 21;
Pred. No. 0.00059;
                                                                                                                                                                                                                                                                                                Human lactoferrin derived peptide SEQ ID NO:47.
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                                                                      Mismatches
                                                                                                                                                                                                      AAY78047 standard; Peptide; 12 AA.
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                                        90.6%;
91.7%;
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98SE-0004614.
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29-DEC-1998;
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AAY78037 standard; Peptide; 13 AA.

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food such as undant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food, infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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                                                                                                                                                                                                                    Human lactoferrin derived peptide SEQ ID NO:96.
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                                                                                                                AAY78096 standard; Peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                      bactericidal; preservative.
                                                                                                                                                                                  (first entry)
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1 CFQLQRNMRKVR 12
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the inding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or prevention of infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides he used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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91.7%; Pred. No. 0.00064;
ive 0; Mismatches 1; Indels
                                                                                                   Human lactoferrin derived peptide SEQ ID NO:37.
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                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                    99WO-SE01230.
                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AA;
                                                                                                                                                                                                                                                                              WO200001730-A1.
                                                                                                                                                                                                                             Homo sapiens.
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                   06-JUL-1999;
                                                                  25-APR-2000
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                                                                                                                                                                                                                                               Synthetic.
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Best Local S
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Gaps

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Best Local Similarity 83.3 Matches 10; Conservative

Matches

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RESULT 7

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammartions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula so be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammartory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower entire them to be used for the same purposes as lactoferrin at lower
               Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colltis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90.6%; Score 58; DB 21; Length 13; 91.7%; Pred. No. 0.00064; rive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 15; Page 74; 102pp; English
                                                                                                                                                                                                                                                  99WO-SE01230.
                                                                                                                                                                                                                                                                                    98SE-0002441.
                                                                                                                                                                                                                                                                                                                         98SE-0004614
                                                                           bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                             (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 AA;
                                                                                                                                                                     WO200001730-A1
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                                                                                                                                                                                                                                                                                                      17-JUL-1998;
29-DEC-1998;
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                                                                                                                                                                                                           13-JAN-2000
                                                                                                                                Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candia infection an a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canbe them to be used for the same purposes as lactoferrin at lower

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 18; Page 74; 102pp; English

Baltzer L,

Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB.

98SE-0002441. 98SE-0004614.

06-JUL-1998; 06-JUL-1999;

29-DEC-1998;

99WO-SE01230

WO200001730-A1

Synthetic.

13-JAN-2000

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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                                                                                                                                                AAY78036 standard; Peptide; 14 AA.
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Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                            1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                          2 CFOWORINMRKVR 13
                                                                                                                                                                                                                                                                                                Sequence 13 AA;
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0; Gaps

11; Conservative

Matches

Best Local Similarity

1 CFOLORNMRKVR 12 CPOWORNMRKVR 13

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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

Human lactoferrin derived peptide SEQ ID NO:49.

(first entry)

25-APR-2000

AAY78049;

AAY78049 standard; Peptide; 13 AA.

AAY78049

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Dolphin GT;

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AAY78050 standard; Peptide; 14 AA.
                                                          Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                            98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                                                                        Conservative
                     (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                      1 CFOLORNMRKVR 12
                                      WPI; 2000-147388/13.
                                                                                                                                       Sequence 14 AA;
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29-DEC-1998;
        17-JUL-1998;
29-DEC-1998;
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                             Hanson LA,
                                                                                                                                                                                                                                                          Synthetic
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infections and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                       AAY78001 to AAY78100 represent peptides having sequences based on human
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                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                Claim 15; Page 75; 102pp; English.
  Hanson LA, Mattsby-Baltzer I,
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98SE-0002562.
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Matches 11; Conservative
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                                           WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14 AA;
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                                                                                                                                                                                                                                                                                                                                                                  AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through brinding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also funginidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
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food, infant formula, anti-inflammatory, anti-microbial, anti-tumour;
urinary tract infection, colitis, Candida infection, fungicidal;
bactericidal, preservative.
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                                                                                                                                                                     Baltzer L, Dolphin GT;
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                                                                                                                                                                  Mattsby-Baltzer I,
                                                     98SE-0002562.
98SE-0004614.
                               98SE-0002441.
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB.

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Claim 18; Page 75; 102pp; English,

AAY78035 standard; Peptide; 15 AA.

RESULT 14

AAY78035

AAY78035;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also the fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
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                                                                                                                                                                                                                                                                                                                 Length 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.6%; Score 58; DB 17; Length 15; 91.7%; Pred. No. 0.00074; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              anti-ulcer agent; low toxicity; stable; heat-resistant.
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                                                                                                                                                                                                                                                                                                              Score 58; DB 21;
Pred. No. 0.00069;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                90.68;
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                  14 AA;
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CFQLQRNMRKVR

2 CFÓWÓRNMRKVR 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production coets. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dolphin GT;
                                                                                   Human lactoferrin derived peptide SEQ ID NO:35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 69; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                 99WO-SE01230.
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                                                 25-APR-2000 (first entry)
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                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1998;
                                                                                                                                                                                                                                                                                             13-JAN-2000
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                                                                                                                                                                                                                           Synthetic
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AC AAY7
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lactoferrin. The population are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                               Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                    Human lactoferrin derived peptide SEQ ID NO:62.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 15; Page 81; 102pp; English.
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98SE-0002562.
98SE-0004614.
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                                         25-APR-2000 (first entry)
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17-JUL-1998;
29-DEC-1998;
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Dolphin GT;

Gaps . 0 / Match 90.6%; Score 58; DB 21; Length 15; Local Similarity 91.7%; Pred. No. 0.00074; Hoss 11; Conservative 0; Mismatches 1; Indels Query Match Matches

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1 CFOLORIMRKVR 12

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4 CEÓWÓRNMRKUR 15

Search completed: February 21, 2003, 07:37:14 Job time : 29.35 secs

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NAME/KEY: Peptide
LOCATION: 1.18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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US-08-204-487-3
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                                                                           February 21, 2003, 07:25:59 ; Search time 8.65 Seconds
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2: /cgn2_6/ptcdata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptcdata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptcdata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1,3
(c) 1993 - 2003 Compugen Ltd.
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US-08-485-948-8

US-08-475-055-8

US-07-755-161A-3

US-07-891-174-3

US-08-204-487-1

US-08-256-771-25

US-08-381-984-25

US-08-381-984-25

US-08-381-984-25

US-09-508-771-25

US-09-508-734-6

US-09-508-734-6

US-07-755-161A-10

US-07-755-161A-8

US-07-755-161A-8

US-07-891-174-8

US-07-891-174-8

US-07-891-174-8

US-07-891-174-8

US-07-891-174-8

US-07-891-174-8

US-07-891-174-8

US-07-9508-734-8

US-07-9508-734-8

US-07-9508-734-8

US-07-9508-734-8

US-07-9508-734-8

US-07-9508-734-8

US-08-204-487-7

US-08-204-487-7

US-08-204-487-7

US-08-204-487-7
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                                                                                                                                                                                                                       262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 OM protein - protein search, using sw model
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Maximum DB seq length: 200000000
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Match Length DB
          Copyright
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APPLICANT: TARAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MANAKA, SHIGBARU
APPLICANT: TANAKA, SHIGBARU
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: DOSAKO, SHUN'ICHI
TITLE OF INVENTION: VIRAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MORDURAL INTERPRETATION:
MORDURAL: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INPORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 83,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAN: (617) 248-7000
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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CHARACTERISTICS:
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CHARACTERISTICS:
CHARACTERISTICS:
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ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
         US-08-406-271-2
US-08-745-586-2
US-09-932-190-2
US-09-932-190-2
US-08-655-640-4
US-08-655-640-4
US-08-461-333-4
US-08-461-333-4
US-09-461-333-4
US-09-466-167-4
US-09-476-798-4
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US-08-456-108-2
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MEDIUM TYPE: Floppy disk
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GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAMI
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TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE: NO FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                            CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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                                       RESULT 3
US-08-628-380-8
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APPLICANT: TONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAIN
TITLE OF INVENTION: ACBNTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
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90.6%; Score 58; DB 2; Length 18;
Best Local Similarity 91.7%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                      Score 58; DB 1; Length 18;
Pred. No. 0.00037;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION 1436
FRIDG APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY, AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1879-5800
                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08485948
Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 Hackensack Avenue
OTHER INFORMATION: (20-37) "
                                                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
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CITY: Hackensack
STATE: New Jersey
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                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: YONG M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL:
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TELEX: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-485-948-B
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US-08-485-948-8
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US-08-204-487-3
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PRETENCE APPLICATION US / 08628380

PRETENCE APPLICANTY ULSARA, HELEN
PRETENCE APPLICANTY ULSARA, HELEN
PRICANTY ULSARA, HELEN
PRICANTY ULSARA, HELEN
PRICANTY ULSARA, HELEN
PRICANTY ULSARA, HELEN
ADDERSE: ALABDE & Jackson
ADDERSE: ALABDE & Jackson
ADDERSE: ALABDE & Jackson
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: REAL RECORDS APPLICATION
FOR THE REAL RECORDS APPLICATION
COUNTRY: USA
COUNTRY: WAS ADDERSE: USA
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90.6%; Score 58; DB 1; Length 20;
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FILING DATE:
PRILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                 FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFREENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8850
                                   OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: modified site
                                                  SOFTWARE: DisplayWrite CURRENT APPLICATION NUMBER: US/
                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Li
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TISSUE TYPE:
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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL:
VOLUME:
ISSUE:
PAGES:
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Pred. No. 0.00037;
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APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
FAPLICATION NUMBER: 08/485,948
FILING DATE: 07/1595
FILING DATE: 07/1595
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
ATTONNEY,FAGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5800
TELEFRAX: 201 343-1684
AUDRESS:
ALRET: Klauber & Jackson
CITY: 411 Hackensack
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 0761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
US-07-755-161A-3
p. Sequence 3, Application US/07755161A
patent No. 5304633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 90.6%;
Best Local Similarity 91.7%;
Matches 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             internal
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US-08-475-055-8
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LOCATION: 19
IDENTIFICATION WETHOD:
COTHER INFORMATION: (ye residue at location 19 connected by disulfide bond with OTHER INFORMATION: (ye residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of (ye residue at location 2" AUTHORION: AUTHORS:
AUTHORS:
UNITS:
NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION: Anote= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
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LOCATION: 19
IDBNITICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
AUTHORS:
TITLE:
                                      OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19" FERAUNE:
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APPLICANT: NAKAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MATARA, HIDEKI
APPLICANT: MATARA, SHIGBARI
APPLICANT: TANARA, SHIGBARI
APPLICANT: TOSHAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIARI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: ADDRESSEE: THIBEAULT
ADDRESSEE: THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 58; DB 1; Length 20;
Pred. No. 0.00042;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE FOOKET NUMBER: PJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUBLICATION DATE: RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 1, Application US/08204487; Patent No. 5565425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.68;
                                                                                                                          NAME/KEY: modified site
LOCATION: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 90.6
Best Local Similarity 91.7
Matches 11; Conservative
  LOCATION: 2
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOLORNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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STREET: 53
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                                                                                                                                                                                                                                                                                                                            JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-891-174-3
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Best Local Similarity 91.7%; Pred. No. 0.00042;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                    Sequence 3. Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified site
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TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
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CHROMOSOME/SEGMENT:
MAP POSITION:
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                                                                 1 CFQLQRNMRKVR 12
                                                                                                          2 CPOWORNMRKVR 13
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LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washi
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CELL TYPE:
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                                                                                                                                                                       RESULT 6
US-07-891-174-3
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RESULT 9
US-08-256-771-25
S Gequence 25, Application US/08256771
Patent No. 5656591
Targent of Septement of S
                                                                                                    Query Match
90.6%; Score 58; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00042;
Matches 11; Conservative 0; Mismatches 1; Indels
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771.
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY AGENT INFORMATION:
NAME: WARTEN M. Cheek, JE.
REGISTRATION NUMBER:
REGISTRATION NUMBER:
REGISTRATION NUMBER:
NAME: WASTEN M. Cheek, JE.
REGISTRATION NUMBER:
REGISTRATION NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 25: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 20 amino acida
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                      1 CFQLQRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQLQRNMRKVR 12
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Best Local Similarity
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US-08-381-984-24
              US-08-256-771-24
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Patent No. 565591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
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OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Peptide
COCATION: 1..20
COCHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS
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STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
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ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET UNBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/25
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS; single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 24:
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nes 11; Conservative
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOLORINMRKVR 12
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US-08-256-771-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-204-487-1
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ch 90.6%; Score 58; DB 1; Length 20; 1 Similarity 91.7%; Pred. No. 0.00042; 11; Conservative 0; Mismatches 1; Indels
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us-09-743-107b-80.rai

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OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment there
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OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVANTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
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                                                                                                             COMPUTER ERADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: April 11, 1995
       805 Fifteenth Street, N.W., #700
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CURRENT FILING DATE: 2000-66-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1999-07-14
PRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SEQ ID NO 4
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; Patent No. 6423509
                                                                                                                                                                                                                                                                                             CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Walren M. Cheek, Jr.
REGISTRATION NUMBER:
TELERRENCE/DOCKET NUMBER:
TELERRENCE/ORGINION INFORMATION:
TELERRENCE/20071-8850
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SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
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                              Washington
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                                                                                               20005
                                                  STATE: D.C COUNTRY: U
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OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
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                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: LibM Compatible
COMPUTER: LibM Compatible
OPERATING SYGTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
                                                                                                                                                               ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
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Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
Sequence 24, Application US/08381984 Patent No. 5804555 GENERAL INFORMATION:
                                                                     APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best_Local Similarity 91.7
Matches 11; Conservative
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IDENTIFICATION METHOD:
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APPLICATION NUMBER:
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MOLECULE TYPE: peptide
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STRANDEDNESS: B11
                                                                                                                                                                                                                               STATE: D.C. COUNTRY: U.S.A.
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US-08-381-984-25
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FRATURE:
NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: (ys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION DATE:
; RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                       NAME: Warren M. Cheek Jr. REGISTRATION NUMBER: 33,367
                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INPORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-885
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LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys re
OTHER INFORMATION: Cys re
                        ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
IARGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
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CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBBARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOCUMENT NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
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Sequence 6, Application US/09508734

Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: useful microorganism thereof

CURRENT PAPLICATION NUMBER: US/09/508,734

CURRENT PAPLICATION NUMBER: PCT/KR99/00373

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-13

NUMBER OF SEQ ID NOS: 12

SEQ ID NO 6

LENGTH: 24

TYPE: PRIOR PAPLICATION NUMBER: TOTAL SEQ ID NO 6

LENGTH: 24

TYPE: PRIOR PAPLICATION NUMBER: TOTAL SEQ ID NO 6

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TYPE: TOTAL SEQ ID NO 6

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                                                                                                                                 90.6%; Score 58; DB 4; Length 22; 91.7%; Pred. No. 0.00046; Live 0; Mismatches 1; Indels
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US-07-755-161A-10
US-07-755-161A-10
US-07-755-161A-10
Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
APPLICANT: Wamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
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MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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milarity 91.78;
Conservative
                                                                                                                                 Query Match 90.6
Best Local Similarity 91.7
Matches 11; Conservative
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                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOLORNMRKVR 12
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LENGTH: 22
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Gaps ; 0

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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
PUBLICATION INFORMATION:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
90.6%; Score 59; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 0.00052;
Matches 11; Conservative 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQLQRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-891-174-10
                                                                                                                                                                                                                                                                        JOURNAL:
                                                                                                                                                                                                                                                                                                      VOLUME:
                                                                                                                                                                                                                                                                                                                                                                             PAGES:
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LOCATION: 4
LOCATION: 4
CTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 21"
                                                    VESOUR 12

VESOUR 12

Sequence 10, Application US/07891174

Patent No. 5317084

Patent No. 5317084

Patent INVEMATION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS: 10

CORRESPONDENCE ADDRESS: 400

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington STREET: 805 Fifteenth Street, N.W., #700

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

COMPUTER: IBM Compatible COMPINE TRADBLE FORM: MS-DOS

SOFTWARE: Diskette, 5.25 inch, 500Kb

COMPUTER: IBM Compatible COMPINES: 105playWrite

COMPUTER: Diskette, 5.25 inch, 500Kb

COMPUTER: DISPLAYMITE

APPLICATION NUMBER: US/07/891,174

FILING DATE: 05-SEP-1991

ATTORNEY AGENT INPORMATION:

APPLICATION NUMBER: 33,367

RESPERENCE/DOCKET NUMBER:

TELEPROMUNICATION INFORMATION:

TELEBROMUNICATION INFORMATION:

TELEBROMUNICATION INFORMATION:

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SEQUENCE CHARACTERISTICS:
LIBNGTH: 25 amino acids
TYPE: amino acid
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NAME/KEY: modified site
LOCATION: 21
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CHROMOSOME/SEGMENT:
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FEATURE:
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DEVELOPMENTAL STAGE:
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CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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574, App
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Sequence 20, Appl
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35.508 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-798-869-23
US-09-738-626-5597
US-09-829-378-7
US-10-013-310-5
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US-09-798-869-20
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US-09-798-869-6
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App	App		
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557-5	700-5	572-5	579-5	582-5	588-5	739-5	740-5	743-57	488-57	492 - 5	747-57	750-57	-985-5	987-57	991-57	992-5	993-57	658-57	695-5	-697-57	.705-5	-915	-585-	586-5	-747-574	SINIS	
0	-0	0	-01	-01	-0	10-175	-0	10-175	10-176	10-176	10-176	10-176	-6	10-176	6	10-176	10-176	-184	10-173	-01	10-173	-01	-01	2	10-175	ALIGNMENTS	
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3	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35	35		
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45		

GENERAL INFORMATION: US/0979869
; Publication No. US20030022821A1
; GENERAL INFORMATION: SIGURD SYENDSEN
APPLICANT: (YSTEIN REKUAL
APPLICANT: (YSTEIN REKUAL
APPLICANT: LARS VORIAND
TILLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASESEQ for Windows Version 4.0 US-09-798-869-2

Gaps ; 0 90.6%; Score 58; DB 9; Length 15; 91.7%; Pred. No. 6.7e-05; tive 0; Mismatches 1; Indels 11; Conservative Best Local Similarity Query Match Matches

ORGANISM: HOMO SAPIENS

SEQ ID NO 2 TYPE: PRT

LENGIH:

US-09-798-869-2

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1 CFQLQRNMRKVR 12 CFOWORNMRKVR 14 à ď

Sequence 20, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: RALDUR SVEINBJ (RNSSON RESULT 2 US-09-798-869-20

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0-698-867-60-SD
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APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                        90.6%; Score 58; DB 9; Length 25; 91.7%; Pred. No. 0.00011; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Jacobson, Price, Holman & Stern 400 Seventh St. N.W.
           TITLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
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APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Player, William E. REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEPAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 694 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Y: U.S.A.
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LARS VORLAND
                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQLQRNMRKVR 12
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Best Local Similarity
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ch 90.6%; Score 58; DB 9; Length 694; l Similarity 91.7%; Pred. No. 0.0035; ll; Conservative 0; Mismatches 1; Indels
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JOS-09-798-88-93

JOS-09-798-88-93

JUDIcation No. US20030022821A1

GENERAL INFORMATION:

JAPPLICANT: JOHN SIGHED SYENDEN

APPLICANT: (YSTEIN REXDAL

APPLICANT: ALDUR SVEINBU RNSSON

APPLICANT: BALDUR SVEINBU RNSSON

APPLICANT: ALAS VORLAND

TILLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 1999-08-31

FRIOR APPLICATION NUMBER: GB9918938.4

PRIOR APPLICATION NUMBER: GB9918938.4

PRIOR APPLICATION NUMBER: GB9918938.4

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 15
                                                                                                                                                                                                                                         ; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.3%;
Matches 10; Conservative
                                                                              1 CFOLORNMRKVR 12
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    Query Match
Best Local Similarity
Matches 11; Conserv
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Fatent No. US2020170082A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
FILE REFERENCE: 033229/0631
CURRENT APPLICATION NUMBER: US/09/829,378
CURRENT APPLICATION NUMBER: US/09/829,378
FILE REFERENCE: 033229/0631
CURRENT APPLICATION NUMBER: US 09/340,684
PRIOR PILING DATE: 2001-05-09
PRIOR PAPEL DATE: 2001-06-01
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56.2%; Score 36; DB 9; Length 360; 54.5%; Pred. No. 23;
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               59.4%; Score 38; DB 9; Length 97; 70.0%; Pred. No. 2.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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                                                     1; Mismatches
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CURRENT APPLICATION NUMBER: US/10/013,310
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: PCT/GB00/02191
PRIOR PILING DATE: 2000-06-05
PRIOR PILING DATE: 1999-06-08
PRIOR APPLICATION NUMBER: UK 9913350.6
PRIOR APPLICATION NUMBER: UK 9921953.7
PRIOR FILING DATE: 1999-06-08
NUMBER OF SEQ ID NOS: 8
SEQ ID NO 5
LENGTH: 700
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APPLICANT: Hoyne, Gerard Francis
APPLICANT: Dallman, Margaret Jane
IITLE OF INVENTION: Therapeutic Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 5, Application US/10013310; Publication No. US20020192216A1; GENERAL INFORMATION:
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                                                       7; Conservative
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US-09-829-378-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: House Mouse US-10-013-310-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                 Best Local Similarity
Matches 7; Conserva
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Best Local Similarity
Matches 6; Conserv
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73 CFLVQRNNRK 82
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US-09-829-378-7
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                   Query Match
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Pred. No. 0.17;
2; Mismatches 2; Indels
   2; Indels
   2; Mismatches
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TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSESEE FOR Windows Version 4.0
SEQ ID NO 23
LENGTH: 25
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CURRENT FILING DATE: 2000-12-18
PRIOR PELLING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SOFTWARE: Patentin ver. 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5597, Application US/09738626; Publication No. US20020197605A1; GENERAL INFORMATION:
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5597
                                                                                                                                                                   ; Sequence 23, Application US/09798869; Publication No. USCO30022821A1; GENERAL INFORMATION: APPLICANT: JOHN SIGURD SVENDSEN
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APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
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63.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Conservative
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                                     1 CFQLQRNMRKV 11
                                                               3 CYQWQRRMRKL 13
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US-09-798-869-23
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US-10-173-706-574
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US-10-175-737-574
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME CURRENERNE: P3430R1C104
CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT PILING DATE: 2002-06-21
                                                                                                                                                                                                                                                                APPLICANT: Pan, James
APPLICANT: Smith, Victoria
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Watanabe, Colin K.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACTIOS ENCODING THE SAME FILE REFERENCE: P3430R1C42
CURRENT APPLICATION NUMBER: US/10/174,590
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
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SEQ ID NO 574
LENGTH: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 574, Application US/10176758; Publication No. US20030008353Al GENERAL INPORMATION: APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
                                                                              Sequence 574, Application US/10174590 Publication No. US20030008352A1 GENERAL INFORMATION:
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Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
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Best Local Similarity 54.5
Matches 6; Conservative
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Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                                              APPLICANT: Baker, Kevin P. APPLICANT: Chen, Jian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
CRGANISM: Homo Sapien
US-10-174-590-574
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US-10-176-758-574
                                              RESULT 10
US-10-174-590-574
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LENGTH: 882
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APPLICANT:
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SCREETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C7
CURRENY EPPLICATION NUMBER: US/10/173,706
CURRENY FILING DATE: 2002-06-17
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 574
LENGTH: 882
                                                                                                                                                                                                                                                                                   APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 574
LENGTH: 882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    54.7%; Score 35; DB 9; Length 882; 54.5%; Pred. No. 89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 574, Application US/10173706; Publication No. US20030022293A1; GENERAL INFORMATION:
; Sequence 574, Application US/10175737; Publication No. US20030013153A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Desnoyers, Luc
Goddard, Audrey
Goddwski, Paul J.
Gurney, Austin L.
Pan, James
Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
Gurney, Austin L.
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CRGANISM: Homo Sapien
US-10-173-706-574
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; ORGANISM: Homo Sapien
US-10-175-737-574
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US-10-175-752-574
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CURRENT APPLICATION NUMBER: US/10/175,752
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 574
LENGTH: 882
                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERBRNCE 1943 ORLC45
CURRENT APPLICATION NUMBER (US/10/175,738
CURRENT APPLICATION NUMBER (US/10/175,738
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 574
LENGTH: 882
TYPE: RRT
CORGANISM: Homo Sapien
US-10-175-738-574
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                     2; Indels
   54.5%; Pred. No. 89;
tive 3; Mismatches
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Publication No. US20030022294A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Chen, Jian
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Goddard, Audrey
Goddwski, Paul J.
Gurney, Austin L.
Pan, James
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Matanabe, Colin K.
Wood, William I.
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Smith, Victoria
Watanabe, Colin K.
Wood, William I.
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Gurney, Austin L.
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ORGANISM: Homo Sapien
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848 CEQVDRNIRRV 858
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 Best Local Similarity
Matches 6; Conserva
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US-10-175-752-574
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US-10-175-738-574
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55 ; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-80 64 Title: Perfect score:

1 CFQLQRNMRKVR 12 Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 segs, 96134422 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	lactotransferrin p	probable peroxisom	hypothetical prote	•	ĭ	lactoferrin - shee	_		_	_	_	hypothetical prote	hypothetical prote	probable transcrip	hypothetical prote	hypothetical prote	arginyltransferase	chalcone synthase	secY protein - red	hypothetical prote	glycolate oxidase	probable potassium	teichoic acid bios	probable membrane	ATP-dependent deox	hypothetical prote	hypothetical prote	_	_
3 ID				2 JC2323		2 S52107	2 T33211				2 A96516	2 A97524	2 AB2743	2 G64908	2 B85720	2 E90897	2 AI3401	2 T03612	2 S47440	2 AG2342	2 T31292	2 T28852	2 AE1210	2 S49965	2 A39432	2 T29970	D8194	2 E95172	2 E98038
Length DB	711																			508	19		969			_		_	81
Query Match	0	64.1	64.1	64.1	62.5	59.4	59.4	57.8	57.8	57.8	57.8	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.2	56.3	56.2	56.2	56.2	56.2	56.2	54.7	54.7	54.7	54.7
Score	58	41	41	41	40	38	38	37	37	37	37	36	36	36	36	36	36	36	36	36	36	36	36	36	36	35	35	35	35
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hypothetical prote	hypothetical prote	60S ribosomal prot	ribosomal protein	hypothetical prote	hypothetical prote	hypothetical prote	probable malate de	malate oxidoreduct	hypothetical prote	embryogenic callus	probable ribonucle	hypothetical prote	2-amino-4-hydroxy-	protein ZK1073.2 [hypothetical prote
D95003	E71547	T00407	A42840	T15387	S77802	D86255	A81933	C81173	S50977	T49924	F81411	T34468	F72425	F89732	D71436
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104	151	159	179	234	267	295	426	426	431	445	644	795	129	189	273
54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	54.7	53.1	53.1	53.1
35	35	35	35	35	35	35	35	35	35	35	35	35	34	34	34
30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

ALIGNMENTS

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lactotransferrin precursor [validated] - human
N.Alternate names: lactoferrin
C.Species: Homo sapiens (man)
C.Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C.Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74 R;Cho, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNÅ
A; Residues: 1-711 < CHO>
A; Cross-references: EMBL:U07643; NID:g467236; PIDN: AAB60324.1; PID:g467237
R; Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nicoleic Acids Res. 18, 5288, 1990
A; Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A; Reference number: S11228; MUID:90384839; PMID:2402455
                                                                                                                                                                                                                                                                                                           súbmitted to the EMBL Data Library, March 1994
A; Afeference number: G06820
A;Accession: G01394
A;Status: preliminary; translated from GB/EMBL/DDBJ
RESULT 1
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A; Accession: S11228

A; Molecule type: mRNA A; Meadudes: 1-148, Tr.,150-422, Cr.,424-711 <REY>
A; Cross-references: EMBL.X53961; NID:934415; PIDN:CAA37914.1; PID:934416
B; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
R; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
A; Title: 0; 1969-11981, 1992
A; Title: Differential molecular mechanism of the estrogen action that regulates lactofer: A; Reference number: A45401; MUID:93125571; PMID:1480183

A;Accession: A45401 A;Molecule type: DNA A;Residues: 1-15 <TEN>

A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A;Experimental source: placentá A;Note: sequence extracted from NCBI backbone (NCBIP:122202) R;Powell, M.J.; Ogden, J.E. Nucleic Acids Res. 18, 4013, 1990 A;Title: Nucleotide sequence of human lactoferrin cDNA. A;Reference number: S10324; MUID:90326549; PMID:2374734

A, Accession: S10324

A, Molecule type: mRNA A, Readudes: 3-711 < ROBES A, CCOSE-references: ENBL: X22941; NID: 934411; PIDN: CRA37116.1; PID: 934412 A, CCOSE-references: ENBL: A.; Funk, W.D.; Tweedie, J.W. B; Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W. Biochem J. 276; 349-355; 1991 A; Title: Expression of cloned human lactoferrin in baby-hamster kidney cells. A, Reference number: S15853; MUID: 91264786; PMID: 2049066

A; Status: nucleic acid sequence not shown; not compared with conceptual translation A;Accession: S15853

A; Molecule type: mRNA A; Residues: 20-31 <ST1>

A; Accession: S20841

A; Molecule type: protein A; Residues: 20-28,'X',30-31 <ST2>

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64.1%;
41.7%;
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155 CYELQQNSKKIK 166
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                     A; Map position: 1
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H96515
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A, Residues: 20-140,142-169 171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4,
A, Residues: 20-140,140-169 171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4,
A, Note: this is the final paper in a series
B, Hoeddall, B.V.; Barkholt, V.; Norskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A, Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A, Reference number: 874119; MUID:97054624; PMID:8898921
A, Accession: 874119
A, Residues: 'G', 22-24', R', 26-27', XX', 30-32 < HOUS
A, Residues: 'G', 22-24', R', 26-27', XX', 30-32 < HOUS
A, Experimental source: neutrophil granulocytes
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F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e

F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e

F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental

F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                                                                     A; Molecule type: m.NA
A; Residues: 436-487, 24,489-711 <RAD>
A; Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
A; Panella, T.J.; S037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 3-701, SWKPVN APNA
A;Residues: 3-701, SWKPVN APNA
A;Experimental source: normal breast tissue
R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Br. J. Blochem: 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A;Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                         É
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Accession: S07160
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Pred. No. 0.0053;
0; Mismatches 1; Indels
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A;Map position: 3421-3423
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; tron binding; milk
C;Keywords: duplication; glycoprotein; iron binding; milk
F;1.13/Domain: signal sequence #status predicted <21G>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90.68;
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A; Residues: 1-223 <MUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A31000
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Rice Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
Arithe. Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A; Reference number: JC2323; MUID:94380047; PMID:8093048
A; Accession: JC2323
A; Molecule type: mRNA
A; Residues: 1-708 < LEP>
C; Superfamily: transferrin; transferrin repeat homology
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F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cispecies: Schizosaccharomyces pombe
Cidate: 03-Dec-1999 #sext_change 28-Jul-2000
Cidate: 03-Dec-1999 #sext_change 28-Jul-2000
Cidates: 03-Dec-1999 #sext_change 28-Jul-2000
Cidates: 03-Dec-1999 #sext_change 28-Jul-2000
Cidates: 174056
R;Wood, V; Rajandream, M.A.; Barrell, B.G.; Davis, P.; Churcher, C.M.
A;Reference number: Z21937
A;Reference number: Z21937
A;Reference number: Z1937
A;Reference number: July 1999
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-238 < WOO>
A;Cross_references: EMBL:AL096788; PIDN:CAB46672.1; GSPDB:GN00067; SPDB:SPBC582.09
A;Cross_references: EMBL:AL096788; PIDN:CAB46672.1; GSPDB:GN00067; SPDB:SPBC582.09
C;Genetics: Continue of the continue of
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein SPBC582.09 - fission yeast (Schizosaccharomyces pombe)
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A;Introns: 10/3; 170/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
C;Keywords: peroxisome
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A;Introns: 15/3; 25/3; 185/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
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                                                                                                                                                                                                                                                                       Length 223.
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Pred. No. 2.9;
6; Mismatches
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hypothetical protein b2984 - Bscherichia coli (strain K-12)
C;Species: Bscherichia coli
C;Species: Bschoris F65084
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co. A; Rose, D.J.; Mau, B.; Shao, Y.
Science D.J.; Mat, B.; Shao, Y.
Science number: Ascherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rikaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; MUID:21595285; PMID:11759840
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AH1866
    A;Cross-references: EMBL:AF067944; PIDN:AAC17673.1; GSPDB:GN00023; CESP:K10C9.6
A;Experimental source: strain Bristol N2; clone K10C9
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A;Experimental source: strain PCC 7120
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                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein all0481 [imported] - Nostoc sp. (strain PCC 7120)
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                                                                            A,Gene: CESP:KIOC9.6
A,Map postition: 5
A;Introns: 163/2; 313/1
C,Superfamily: Caenorhabditis elegans hypothetical protein C45H4.12
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 187;
                                                                                                                                                                                               59.4%; Score 38; DB 2; Length 335; 60.0%; Pred. No. 16;
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                                                                                                                                                                                                                                              2; Mismatches
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B; Conservative
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168 FELPTNMRKMR 178
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                                                                                                                                                                                                                                                                                                                                         217 CVOMHRNMKK 226
                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-187 <KUR>
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Best Local Similarity
                                                                                                                                                                                                                                                                                               1 CFQLQRNMRK 10
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                                                           C;Genetics:
                                                                                                                                                                                                                                                   Matches
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lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Decies: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S2107
R;Oian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Pitle: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Accession: S52107; MUID:95127729; PMID:7827104
A;Accession: S52107
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A, Molecule type: DNA
A, Residues: 1-887 <STO>
A, Cross-references: GB: AE005173; NID: 95668806; PIDN: AAD46032.1; GSPDB: GN00141
C, Genetics:
A, Gene: F16N3.18
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C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 08-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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18;
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Pred. No. 1.7;
3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <DUZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 40;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.5%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6; Conservative
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A,Residues: 1-33 <QIA>
C,Superfamily: transferri
C,Keywords: duplication
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Best Local Similarity
Matches 6; Conserv
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Genetics:

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probable transcription regulator ydfH - Escherichia coli (strain K-12)
Schecias: Escherichia coli
C;Specias: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
C;Accession: G64908
R;Blattner, R.R; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Map position: circular chromosome
C,Superfamily: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase; 2-a
                                                                                                                                                                                                                                                                                                                                        A;Gene: AGR C 2500
A;Map positIon: circular chromosome
C;Superfamily: 2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase; 2-a
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R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McCleller, Rarp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: GB:AE000251; GB:U00096; NID:g1787814; PIDN:AAC74613.1; PID:g1787821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein folk [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium A;Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
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A;Residues: 1-153 <KUR>
A;Cross-references: GB:AE007869; PIDN:AAK87146.1; PID:g15156416; GSPDB:GN00169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 01-Feb-2002
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A; Accession: G64908
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-228 <BLAT>
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Local Similarity 41.7%; Pred. No. 21;
Losa 5; Conservative 4; Mismatches 3; Indels
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Best Local Similarity
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A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rithors: School M. R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Crassy, T.H.; Dewar, K.; Anster, C. Hughes, B.; Hulzar, L.
Nature 408 Hule-120, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Rizzo, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference number: A86141; MUID:21016719; PMID:11130712
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                                                                                                                                                     hypothetical protein C47A10.6 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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Pred. No. 66;
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A,Introns: 77/2; 154/3; 179/3; 215/3; 281/1; 302/3
                                                                                                                                                                                                                                                                                          R;Basham, V.
submitted to the EMBL Data Library, November 1996
A;Reference number: Z19207
A;Accession: T19980
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A; Residues: 1-887 <STO>
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A;Experimental source: strain K-12, substrain MG1655 C;Genetics:
A;Gene: ydfH
C;Superfamily: hypothetical protein b1540
C;Superfamily: bydothetical protein b1540
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C;Species: Escherichia coli
C;Species: B5720.

B;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew liler, L.; Grotbecck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Title: Genome sequence of enterohemorrhagic Pscherichia coli O157:H7.
A;Accession: B85720
A;Accession: B85720
A;Accession: B85720
A;Accession: B85720
A;Accession: B85720
A;Accession: B85720
A;Cross-references: GB:AE005174; NID:g12515116; PIDN:AAG56222.1; GSPDB:GN00145; UMGP:Z21
A;Experimental source: strain O157:H7, substrain BDL933

A;Gene: ydfH C;Superfamily: hypothetical protein b1540

; Query Match 56.2%; Score 36; DB 2; Length 228; Best Local Similarity 41.7%; Pred. No. 27; Matches 5; Conservative 5; Mismatches 2; Indels

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Search completed: February 21, 2003, 07:47:53 Job time : 11.65 secs

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Maximum DB
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O9bzf2 homo sapien P10220 herres simp	Q05961 rattus norv P11928 mus musculu	08y052 ralstonia s P10152 bos taurus	Q09688 schizosacch P29996 hepatitis d	Q9fln4 arabidopsis Q58771 methanococc	P55830 drosophila Q9nr22 homo sapien	
ORP7_HUMAN	OAS1_RAT OASA_MOUSE	YB92_RALSO ANGI_BOVIN	YA16_SCHPO	RK27_ARATH YD76_METJA	RS3A_DROME ANM4_HUMAN	
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34	3 8 6 7	8 6	41	4 4	4 4 5 5	

ALIGNMENTS

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Thesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
                                                                                       15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
Lactotransferrin precured (Lactoferrin) (Contains: Lactoferroxin A;
Lactoferroxin B; Lactoferroxin C].
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Mammary gland;
MEDLINE=9034839; PubMed=2402455;
MEY M.W., Woloshuk S.L., de Boer H.A., Pieper F.R.;
"Complete nucleotide sequence of human mammary gland lactoferrin.";
                                                                                                                                                                            homo sapiems (Autazona).
Eukarota; Matazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-Mammary gland;
Liang Q., Jimenz-Flores R., Richardson T.;
"Molecular cloning and sequence analysis of human lactoferrin.";
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Bone marrow; Wei X., Han J., Rado T.A.; "Human neutrophil lactoferrin coding and 5' flanking region DNA
                 TRFL HUMAN STANDARD; PRT; 711 AA.
PO2788; Q16780; Q16785; Q16786; Q16789; O00756; Q9H1Z3; Q96KZ4;
Q96KZ5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
TISSUE-Mammary gland;
Chen K., Huan L.;
Chen K., Huan L.;
submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
TISSUB=Prostate;
Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conneely O.M.; Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 18:5288-5288(1990)
                                                                            Created)
                                                                            (Rel. 01,
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TISSUE=Mammary gland;
                                                                                                                                                                    Homo sapiens (Human)
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                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                          21-JUL-1986
15-JUL-1999
15-JUN-2002
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RESULT 1
TRFL_HUMAN
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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parrell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., La Bastida M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Glacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=90064528; PubMed=2585566;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                  "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of
                                                                                                                                                                                                                                                                                        PRECIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
MEDLINE=82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-82262043; PubMed=7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
Jolles P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W., Baker E.N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE-88001031; Probed-3477300;
Rado T.A., Wei X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
Blood 70:989-993(1987).
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                                                                                                                                   SEQUENCE OP 20-711.

MEDLINE=85076667; PubMed=6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
Legrand D. actorransferrin. amino acid sequence and structural
comparisons with other transferrins.

Eur. J. Blochem. 145:659-666(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haridas M., Anderson B.F., Baker E.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "An 88 amino acid long C-terminal sequence of human
                                                      Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA."; Nucleic Acids Res. 18:4013-4013(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 670:243-254(1981)
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MEDLINE-99190892; Pubmed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97156796; PubMed=9003186;
                        IISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lactotransferrin.";
FEBS Lett. 142:107-110(1982)
                                                                                                                                                                                                                                                                                                                                                                                                             N- and C-terminal domains.";
      SEQUENCE OF 3-711 FROM N.A.
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Council Manage 1973069; Manage 1974, Manage 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                    MEDLINE-99192677; PubMed=10089508; Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.; Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change.";
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-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Agric. Biol. Chem. 54:1803-1810(1990).
                                                                                                                                                                                                                                                                                                                                                                                                Acta Crystallogr. D 54:1319-1335(1998)
                                                                                                                            Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION OF LACTOFERROXINS.
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08-MAR-96.
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1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
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                              ö
                                                                                                                                                                                                                                                                                                                                                               resolution.",
J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AJO10930; CAA09407.1; -.

R PDB; 1B1X; 02-DEC-98.

R PDB; 1B70; 02-EEB-99.

R InterPro; D2-EEB-99.

R InterPro; DR00405; Transferrin. 2.

R PRINTS; PR00422; TRANSFERIN.

R PRINTS; PR00204; TRANSFERIN.

R PROSITE; PS00206; TRANSFERIN 1; 2.

R PROSITE; PS00206; TRANSFERIN 1; 2.

R PROSITE; PS00207; TRANSFERIN 3; 1.

R Signal; 3D-structure.

T NON TER. 4. 6
                                                                                                                                                                                                                                                                                                                                 MEDLINE=99296631; PubMed=10366507;
Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
                              .
0
      90.6%; Score 58; DB 1; Length 711; 91.7%; Pred. No. 0.0014; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Paramasivam M., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLUTAR LOCATION: Secreted.
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                             Matches 11; Conservative
                                                                                                                           STANDARD;
                                                                                                                                                                                                      Equus caballus (Horse).
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695
51
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204
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                                                  1 CFOLORNMRKVR 12
                                                                     39 CPÓWORNMRKVR 50
                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                         TISSUE=Milk;
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         Query Match
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MEDLINE=21848401; PubMed=11859360;

MEDLINE=21848401; PubMed=11859360;

Mod V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,

Sgouros J., Peat N., Hayles J., Basker S., Basham D., Bowman S.,

Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,

Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,

Gentles S., Goble A., Hamilin N., Harris D., Hidalpo J., Hodgson G.,

Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,

James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,

Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,

Mooney P., Moule S., Saunders D., Qeager K., Sharp S.,

Rutherford K., Pearson D., Quail M.A., Rabbinowitsch E.,

Rutherford K., Taylor R.G., Tivey A., Malsh S.V., Marren T., Whitehead S.,

Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mulbert H.,

Meltjens I., Vanstreels E., Rieger M., Schaefer M., Milbert H.,

Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

Beger P., Zimmermann W., Wedler H., Mambutt R., Purnelle B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                              ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.3%; Score 45; DB 1; Length 695; 66.7%; Pred. No. 0.45;
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IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Bukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C582.09 in chromosome II.
SPBC582.09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Mismatches
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Matches 8; Conservative
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                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
Daga R.R., Cruzado L., Jimmez J., Sanchez M., del Rey F., Benito J.,
Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
"The genome sequence of Schizosaccharomyces pombe.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Mammary gland;
Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (JUN-1999) to the EMBL/Genbank/DDBA databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!- SUBBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCLILULAR LOCATION: Secreted.
-!- DOWAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                  Gaps
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Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
NCBI TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                   Score 41; DB 1; Length 238;
Pred. No. 0.85;
                                                                                                                                                                                                                                                                                                                                                 1; Indels
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238 AA; 26479 MW; 58095AA8CD708180 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin)
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last seq
                                                                                                                                                                                                                                                           EMBL; AL096788; CAB46672.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                    64.18;
41.78;
                                                                                                                Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                 5; Conservative
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Best Local Similarity
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Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
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                                                                                                  !ransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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G -> A (IN REF. 2)

S -> P (IN REF. 2)

LLS -> PLF (IN REF. 2)

L -> F (IN REF. 2)

A -> P (IN REF. 2)

A -> P (IN REF. 2)

A -> Q (IN REF. 2)

A -> Q (IN REF. 2)

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A -> P (IN REF. 2)
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IRON 1 (BY SIMILARITY).
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IRON 2 (BY SIMILARITY).
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N-LINKED (GLCNAC.
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                                                                                                                                               LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRFL_CAPHI STANDARD; PRT; 708 AA. (229477; Q29479; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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Interpro, IPR001156; Transferrin.
Pfam, PR00402; TRANSFERIN;
SWART; SW00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00205; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
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38 CAQWQRRMKKVR 49
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Best Local Similarity
8; Conserve
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EMBL; AJ131674; CAB53387.1; -. EMBL; AF165879; AAF82241.1; -.

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Best Local
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BINDING
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 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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Pfam; PF00405; transferrin; 2.
PRINITS; PR00422; TRANSFERRIN.
SMART; SM00942; TR FARFERRIN.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                           TISSUE=Mammary gland;
Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
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LACTOTRANSFERRIN.
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BY SIMILARITY.
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EMBL, X78902, CAA55517.1; -.
HSSP, 077698, ICE2.
                   Bovidae; Caprinae; Capra.
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                                 NCBI TaxID=9925;
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BINDING
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SIGNAL
CHAIN
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METAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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Suzuki K., Takahashi M., Imamura S., Ishikawa T.;
Suzuki K., Takahashi M., Imamura S., Ishikawa T.;
Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: Urea + H(2)0 = CO(2) + 2 NH(3).
-!- COFACTOR: Binds 2 nickel ions per subunit (By similarity).
-!- SUBUNIT: (ALPHA, BETA, GAMMA) (3) (BY SIMILARITY).
-!- PTW: Lys-222 is carbamylated. The carbamoyl group provides the ligands for the two nickel ions (By similarity).
-!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | HSSP; F41.0. | HSSSP; F41.0. | HSSSP; F41.0. | HSSSP; F41.0. | HSSSP; F41.0. | HSSP; F41.0. | 
                                                                                         (POTENTIAL) . (POTENTIAL) . (POTENTIAL) . (POTENTIAL) .
                                            (POTENTIAL)
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01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acid urease alpha subunit (EC 3.5.1.5) (Urea amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 41; DB 1; Length 708;
Pred. No. 2.7;
2; Mismatches 2; Indels
                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTI

I -> V (IN REF. 2) .

C -> K (IN REF. 2) .

C -> K (IN REF. 2) .

F -> P (IN REF. 2) .

F -> P (IN REF. 2) .

D -> G (IN REF. 2) .

D -> G (IN REF. 2) .

W, F2EDBA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus
ANION (BY SIMILARITY).

N-LINKED (GLCNAC. .) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77358 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64.18;
63.68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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        |:| || || 48
CYQWQRRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQLQRNMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDITAR=97188515; PubMed=9037100;
Lewis M.T., Morgan L.W., Feldman J.F.;
Lewis M.T., Morgan L.W., Feldman J.F.;
"Analysis of frequency (frq) clock gene homologs: evidence for a
helix-turn-helix transcription factor.";
Mol. Gen. Genet. 253:401-414(1997).
-!- FUNCTION: CIRCADIAN CLOCK COMPONENT INVOLVED IN THE GENERATION OF
BIOLOGICAL RHYTHMS, IN PARTICULAR IN RHYTHM STABILITY, PERIOD
LENGTH, AND TEMPERATURE COMPENSATION. BEHAVES AS A NEGATIVE
ELEMENT IN CIRCADIAN TRANSCRIPTIONAL LOOP (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FRQ FAMILY.
                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=KIZ / MG1655;
MEDLINE=97426617; PubMed=9278503;
MEDLINE=97426617; PubMett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
"The complete genome sequence of Escherichia coli K-12.";
                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Pungi, Ascomycota, Pezizomycotina, Dothideomycetes,
Pleosporales, Leptosphaeriaceae, Leptosphaeria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%; Score 37; DB 1; Length 252; 57.1%; Pred. No. 5.4; tive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein; ATP-binding; Complete proteome. NP BIND 28 35 ATP (POTENTIAL). SEQUENCE 252 AA; 28151 MW; E9C49E970425C758 CRC64;
046842;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical ATP-binding protein yghR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              992 AA
                                                                                                                                                                                                                                                                                                                                                                                                 sience 277:1453-1474(1997).
!- SIMILARITY: TO E.COLI YGHS AND YGHT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AE000381; AAC76020.1; -. 
EcoGene; EG13002; yghR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 35 A
252 AA; 28151 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U28377; AAA69151.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leptosphaeria australiensis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Frequency clock protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        106 CFSLRRMANLRKVQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQLQR--NMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
Les 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=ATCC 66919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=40116;
                                                                                                                                                                                        NCBI_TaxID=562;
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Q01115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                   Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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    ਨੇ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1411:142-146(1999).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
-!- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
-!- COFACTOR: MAY CONTAIN AN IRON-SULFUR 4FE-4S CLUSTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MADH-ubjquinone oxidoreductase 19.3 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-19.3KD) (CI-19.3KD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MITOCHONDRION (POTENTIAL).
NADH-UBIQUINONE OXIDOREDUCTASE 19.3 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AJ001520; CAA04802...;
InterPro; IPR002096; Cmplx1_20kDa.
Ffam; PR01058; oxidored q6; 1.
PROSITE; PS01150; COMPLEX1_20K; 1.
Oxidoreductase; NAD; Ubiquinone; Mitochondrion; Transit peptide; Iron-sulfur; 4Fe-4S.

MITOCHONDPION (DOWNWART)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sousa R., Barquera B., Duarte M., Finel M., Videira A., "Characterisation of the last Fe-S cluster-binding subunit of Neurospora crassa complex I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37; DB 1; Length 226; Pred. No. 4.8;
                                           Length 573;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3; Indels
                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24972 MW; E48CB09C64AAAFC6 CRC64;
    61805 MW; 2D2619781C39E54B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (4FE-4S)
                                           Score 38; DB 1;
Pred. No. 8.4;
                                                                                                                                                                                                                                                                           226 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRON-SULFUR
                                             59.4%; Score 38; 58.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=99233617; PubMed=10216160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
                                                                                       Conservative
                                                                                                                                                                                                                                                                           STANDARD;
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102
166
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226
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                                                                                                                              1 CFQLQRNMRKVR 12
                       Query Match
Best Local Similarity
7, Conserv?
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226 AA;
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        573 AA;
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ID YGHR_ECOLI
                                                                                                                                                                                                                                                                           NUKM NEUCR
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        SEQUENCE
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METAL
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NUKM NEUCR
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A PARTY A PART

252 AA.

PRT;

STANDARD;

RESULT 8

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Matches

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Gaps

7

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                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                      Biological rhythms; Transcription regulation; Nuclear protein.

DOMAIN 550 554 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).

DOMAIN 868 890 ASP/GLU-RICH (ACIDIC).
                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97426617; PubMed=9278503;
Blatther F. R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blatther F. R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Kriley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
Man B., Shao Y.;
Whe complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474 (1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21074935, PubMed=1120651;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Perna N.T., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Belch R.A., Blattner F.R.;
"Genome sequence of enterchaemorrhagic Escherichia coli 0157:H7.";
Nature 409:529-533 (2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K., Makade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram S., Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T., "A 570-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 28 0-460.1 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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0
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Pred. No. 24;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                     992 AA; 107559 MW; 98E029B585F83AFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P77577;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical transcriptional regulator ydfH.
YDFH OR B1540 OR Z2157 OR ECS2149.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN=0157:H7 / EDL933 / ATCC 700927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97251357; PubMed=9097039;
                                                                                                                                                                                                                                                                                              57.8%;
                                                                                                                                                                   EMBL; U25851; AAB96844.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                        8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                      504 FOLSRDGRKVR 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                               2 FOLORNMRKVR 12
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YDFH ECOLI
ID YDFH ECOLI
                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                      STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=112587)6;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Hayashi T., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.; Scherichia coli "Complete genome sequence of enterohemorrhagic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Rhodophyta, Bangiophyceae, Porphyridiales, Porphyridiaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vogel H., Fischer S., Valentin K.-U., ^{\prime} model for the evolution of the plastid sec apparatus inferred from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                 0157.H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
-!- SIMILARITY: BELONGS TO THE GNIR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00345; HTH GNTR; 1.
PROSITE; PS00043; HTH GNTR FAMILY; 1.
Hypothetical protein; Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.2%; Score 36; DB 1; Length 228; 41.7%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 57 H-T-H MOTIF (POTENTIAL).
228 AA; 26565 MW; 8CFF8BB3BCF9AF84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H-T-H MOTIF (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         746249; Q9MD55;
01-NOV-1995 (Rel. 32, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Preprotein translocase secY subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20496959; PubMed=11040290;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97134960; PubMed=8980520;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      secY gene phylogeny.";
Plant Mol. Biol. 32:685-692(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL, D90798; BAA15246.1; -.
EMBL, D90797; BAA15242.1; -.
EMBL; AE005351; AAGG5222.1; -.
EMBL; AP002557; BAB35572.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000251; AAC74613.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EcoGene; EG13820; ydfH.
InterPro; IPR000524; HTH GntR.
Pfam; PF0032; GntR; 1.
PRINTS; PR00035; HTHGNTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 CYOLEONLHOOR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOLORNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome.
DNA BIND 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN=RK-1;
                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=2771;
                                                                                                                                                                                                                                                                                                                                                                                        REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=RK-1;
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SECY CYACA
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Gaps

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Indels

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"Cloning, sequencing, and expression of Bacillus subtilis genes
involved in ATP-dependent nuclease synthesis.";
J. Bacteriol. 173:3644-3655(1991).
                                     56.2%; Score 36; DB 1; Length 921; 53.3%; Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus subtilis.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
921 AA; 105491 MW; DDFA550E22E846A0 CRC64;
                                                                                                                                                                                                                                                                                                                                  (Rel. 20, Last sequence update) (Rel. 41, Last annotation update)
                                                                                 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98044033; PubMed=9384377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=91267926; PubMed=1646786;
                                                                                                                                                                                                                                                                                                                                  01-NOV-1991 (Rel. 20, Last sequer
15-JUN-2002 (Rel. 41, Last annota
ATP-dependent nuclease subunit B.
                                                                                                                                                                                                                                                                                                                 01-NOV-1991 (Rel. 20, Created)
                                                                                   Conservative
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                647 CFÖLLKNLTCNSKKI 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kooistra J., Venema G.;
                                                                                                                        1 CFQLQRNM----RKV 11
                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=168;
                                                                                                                                                                                                                                                                   ADDB_BACSU
P23477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=OG1;
                                                                                   8
  SEQUENCE
                                           Query Match
                                                                                                                                                                                                                                                   BACSU
                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                    ADDB
                                                                                                                                                                                                                                RESULT 13
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                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                             7. NOI. Evol. 51:382-390(2000).
-!- FUNCTION: INVOLVED IN PROPEIN EXPORT. PROBABLY INTERACTS WITH CHEER PROTEINS TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE CHLOROPLAST ENDOPLASMIC RETICULUM (CER) MEMBRANES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIR=S2B8c / AB972,
STRAIR=S2B8c / AB972,
STRAIR=S2B8c / AB972,
Charcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
                        "The structure and gene repertoire of an ancient red algal plastid
                                                                                                                                              -!- SUBCELLULAR LOCATION: Integral membrane protein. Chloroplast. -!- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Ascomyoota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
116-0CT-2001 (Rel. 40, Last amnotation update)
Hypochetical 105.5 kDa protein in RPL2B-SNL1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein transport; Transmembrane; Chloroplast; Translocation.
CONFLICT 149 H199 MISSING (IN REF. 1).
SEQUENCE 410 AA; 46242 MW; 7CB0130175B1DF03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     921 AA.
      Gloeckner G., Rosenthal A., Valentin K.-U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.2%; Score 36; DB 50.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0303; SECYTRNLCASE.
TIGREPMS; TICR00967; 3a05518007; 1.
PROSTIE; PSO0755; SECY_1; 1.
PROSTIE; PSO0756; SECY_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF022186; AAF12924.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 246881; CAA86975.1; -. SGD; S0001279; YIL017C. Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                         IPR002208; SecY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002208; Si
Pfam; PF00344; secY; 1
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Best Local Similarity
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Matches

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A Kunst F., Ogasawara N., Meszer I., Albertini A.M., Alloni G.,

Kunst F., Ogasawara N., Messeleres P., Bolotin A., Borchert S.,

Ravedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

Borriss R., Boureler L., Brans A., Braun M., Briganell S.C., Bron S.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,

Bronisch F., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,

Bronisch F., Deviner K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,

R. Britz C., Fujita M., Fujita Y., Fuma S., Galisti A., Galiston N.,

R. Aniseppi G., Guy B.J., Haga K., Haisech J., Harwood C.R., Henaut A.,

Guiseppi G., Guy B.J., Haga K., Haisech J., Harwood C.R., Henaut A.,

A Guiseppi G., Guy B.J., Haga K., Haisech J., Harwood C.R., Henaut A.,

A Joris B., Karamata D., Kasabara Y., Klaerr-Blanchard M., Klein C.,

R. Kobyashii Y., Kocetter P., Koningstein G., Krogh S., Kumano M.,

Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,

R. A. Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,

R. A. Noone D., O'Reilly M., Orawa K., Ogiwara A., Oudega B., Park S.H.,

R. A. Seriguchi J., Seconi E., Purnelle B., Rapoport G., Rey M., Sednie S.,

R. Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,

R. Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S.,

R. A. Takeuchi M., Tamakoshi A., Tarakala T., Tarkemaru K.,

R. A. Takadi T., Wanbutt R., Wedler R., Wasarotti A.,

R. A. Takadi K., Wanbutt R., Wadler E., Woshikawa H., Danchin A.,

R. Winters P., Winbat A., Yamamoto H., Yamane K., Yasuwoto K., Yata K.,

R. Winters P., Winbat A., Yamamoto G. the Gram-positive bacterium Bacillus

R. Will F. C., Rocheller B., Waller Gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - FUNCTION: THE ENZYME COMPLEX MAY HAVE A WIDE VARIETY OF CATALYTIC ACTIVITIES INCLUDING ATP-DEPENDENT EXONUCLEASE, ATP-STIMULATED
Noback M.A., Terpstra P., Holsappel S., Venema G., Bron Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
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TISSUB-RELIA, Cerebellum, and Spinal cord;
TISSUB-RELIA, Cerebellum, and Spinal cord;
TISSUB-RELIA, Cerebellum, and Spinal cord;
MEDLINE-20347255; PubMed=10764729;
A Stabach P.R., Morrow J.S.;
Tidentification and characterization of beta V spectrin, a mammalian ortholog of Drosophila beta H spectrin.";
Tortholog of Drosophila Beta H spectra Beta H spectrin.";
Tortholog of Drosophila Beta H spectrin.";
Tortholog of Drosophila Beta H spectra Beta H spectrin.";
Tortholog of Drosophila Beta H spectrin.";
Tortholog of Drosophila Beta H spectra Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A39432; A39432.
Subtilist; BG10465; addB.
InterPro; IPR000212; UvrD-helicase.
Pfam; PF00580; UvrD-helicase; 1.
Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
DNA repair; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                   SUBUNIT: THE B.SUBTILIS ATP-DEPENDENT NUCLEASE COMPLEX IS FORMED BY ONE B SUBUNIT IN CONJUNCTION WITH ONE A SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoitation update)
15-JUN-2002 (Rel. 41, Last amoitation update)
Spectrin beta chain, brain 4 (Spectrin, non-erythroid beta chain 4)
(Beta-V spectrin) (BSPECV).
ENDONUCLEASE, ATP-DEPENDENT HELICASE AND DNA-DEPENDENT ATPASE
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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-!- SIMILARITY: CONTAINS 2 CALPONINY-HOMOLOGY (CH) DOMAINS.
-!- SIMILARITY: CONTAINS 1 PH DOMAIN.
-!- SIMILARITY: CONTAINS 31 SPECTRIN REPEATS.
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EMBL; Y14081; CAA74481.1; -.
EMBL; Z99109; CAB12902.1; -.
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486 FQLQKRMKKAK 496
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Best Local Similarity
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                              Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein.
1 279 ACTIN-BINDING (BY SIMILARITY).
DOMAIN 54 159 CH 1.
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50.0%; Pred. No. 1.5e+02;
ive 3; Mismatches 3;
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SPECTRIN 2.
SPECTRIN 3.
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SPECTRIN 6.
SPECTRIN 7.
SPECTRIN 8.
SPECTRIN 9.
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         entities requires a license agreement (Se or send an email to license@isb_sib.ch).
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SMART; SM00233; PH; 1.
SMART; SM00150; SPEC; 29.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; FALSE_NEG.
PROSITE; PS50021; CH; 2.
PROSITE; PS50003; PH_DOMAIN; 1.
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                                                                  ninerpro; IPR001589; Actbind actuin.
InterPro; IPR001715; Calponin-like.
InterPro; IPR001849; PH.
InterPro; IPR0018017; Spectrin.
InterPro; IPR001605; Spectrin_PH.
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                                  EMBL; AF233523; AAF65317.1; -.
                                                                                                                Pfam; PF00169; PH; 1.
Pfam; PF00307; CH; 2.
Pfam; PF00435; spectrin; 30.
PRINTS; PR00683; SPECTRINPH.
                                           HSSP; Q01082; 1BKR.
Genew; HGNC:15680; SPTBNS.
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2682
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                                                             MIM; 605916; -
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SEQUENCE
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REPEAT
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RESULT 15 RK27_TOBAC

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                                                                                                                                       Nicotiana tabacum (Common tobacco).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                                                                                                              Elhag G.A., Bourque D.P.;
"Nuclear-encoded chloroplast ribosomal protein L27 of Nicotiana
"Abacum: cDNA sequence and malysis of mRNA and genes.";
Biochemistry 31:6856-6864(1992).
-!- SIMILARITY: BELONGS TO THE L27P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.7%; Score 35; DB 1; Length 179; 63.6%; Pred. No. 9.2;
                                        01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
50S ribosoomal protein L27, chloroplast precursor (CL27).
RPL27 OR RPL27A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50S RIBOSOMAL PROTEIN L27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF01016; Ribosomal L27; I.
PRINTS, PR00063; RIBOSOMALL27.
TIGREAMS; TIGR00062; L27; I.
PROSTITE; PS00831; RIBOSOMAL L27; I.
RIBOSOMAL RAMOST.
179 AA.
                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND SEQUENCE OF 52-68.
STRAIN=cv. Petit Havana; TISSUE=Leaf;
MEDLINE=92345244; PubMed=1339289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M75731; AAA34115.1; -.
EMBL; M98473; AAA34104.1; -.
PIR; A42840; A42840.
InterPro; IPR001684; Ribosomal L27.
  PRT;
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SEQUENCE 179 AA; 19664 MW;
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Best Local Similarity 63.6
Matches 7; Conservative
  STANDARD;
  RK27 TOBAC
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152 FRLORERRKAR 162 2 FOLORNMRKVR 12 à

; 0

0; Gaps

3; Indels

1; Mismatches

Search completed: February 21, 2003, 07:27:55 Job time : 5.6 secs

Tue Dec

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OSTCD2
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Q9UCY5
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O61888 caenorhabdi
Q9s6f6 lactobacill
Q8yzh9 anabaena sp
Q9uut7 yarrowia li
O45308 caenorhabdi
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Q9tr80 ovis aries
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Q9sx86 arabidopsis
Q9ltn4 arabidopsis
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Ogssh7 drosophila
                                                                                                                    February 21, 2003, 07:25:55; Search time 20.8 Seconds (without alignments) 118.873 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                       671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
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Listing first 45 summaries
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QBUFP3 QBYGG0 Q43595 Q9VFF6 QBYPAS	086000 Q9N9K2 Q9GYM8 Q8Y833	Q9VR08 Q23578 Q9JV34 Q97PW0	Q97TB1 O59956 Q9H7E7 O84177	022165 Q9VPD0 Q9AWM7 065376 055587	Q9K0D8 Q9JVE6 Q12124 Q9LXD7	Q9FLF7 Q8S1W9 Q9PHN6
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ALIGNMENTS

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Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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0
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                                                                                                                                                                                                                                                                                                                   Strausberg R.; Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; - SEQUENCE 711 Aa; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                  Last annotation update)
                                                                          Last sequence update)
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711 AA
                                                   Created)
  PRT;
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                                         01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
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Best Local Similarity 90.9
Matches 10; Conservative
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PRELIMINARY;
                                                                                                                      Lactotransferrin.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 CFQWQRNMRKV 49
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us-09-743-107b-80.rspt

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SEQUENCE FROM N.A.
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SORETERA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosopila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryota; Moptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                          Gaps
                                                                                              "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                          ó
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                      Score 49; DB 4; Length 38;
Pred. No. 0.018;
0; Mismatches 1; Indels
                                                                                                                                                            InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                        253 AA.
                                                                                                              seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                               MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                          76.6%;
                                                                                                                                                                                                                                           Best Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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                    NCBI_TaxID=9606;
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Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng R.H., Zhong F.N., Zhong F.N., Zhong F.N., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195 (2000).
EMBL; AE003477; ARF4763.1; -
Flybase; Fegno035440; CG14969.
SEQUENCE 253 AA; 27767 MW; DSOBD3A60E0F0428 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=CV. COLUMBIA;
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
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                                                                                                                                                                                                                  Length 253;
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Pred. No.
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(TrEMBLrel. 20, I
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58.3%;
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167 CFDLQDNMNRTR 178
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61.7%; Score 39.5; DB 10; Length 735;

EMBL, AC002304; AAF79335.1; -.
InterPro; IPR001128; CYCchrome_P450.
Pfam; PF00067; P450; 2.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
Heme; Moncoxygenase; Oxidoreductase.
SEQUENCE 735 AA; 84661 MW; 4718F6202974F811 CRC64;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana (Mouse-ear cress).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genomic sequence for Arabidopsis thaliana BAC F14J16 from chromosome
                                                                                                                                                                                                                                                                       Gaps
Lee J., Liu A., Li J., Kremenetskaia I., Gonzalez A., Altafi H., Araujo R., Brooks S., Buehler B., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C., Rowley D., Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.,
                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                           62.5%; Score 40; DB 10; Length 887; 58.3%; Pred. No. 24; ive 2; Mismatches 3; Indels
                                                                                         "Arabidopsis, thaliana chromosome 1 BAC F16N3 sequence."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AC007519; AAD46032.1; -.
Interpro; IPR0020318. EF-hanb; UNKNOWN 1.
PROSITE; PS00018; EF HAND; UNKNOWN 1.
SEQUENCE 887 AA; 100064 MW; 533510830A4A5099 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ecker J.R.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                              735 AA.
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                                                                                                                                                                                                                                                 Local Similarity 58.3
nes 7; Conservative
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Submitted (APR-2000)
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Submitted (AUG-1997)
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Q9LG17
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SEQUENCE FROM N.A.
ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Isogai T., Ota T., Hayashi K., Sugano S., Aotsuka S., Yoshikawa Y.,
Nishikawa T., Nagai K., Sawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Matsunawa H., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A.,
Nakamura Y., Nagahari K., Masuho Y., Sasaki N.;
"NEOO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                   Gaps
                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin (Fragment)
Lactoferrin (Fragment)
Lactoferrin (Fragment)
Eukaryota aries (Sheep)
Bukaryota Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                   Indels
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SEQUENCE 125 AA; 13445 MW; 66AlCDD5774E7BD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32 (1995).
HSSP: 077698; 1CR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update
CDN FL112988 fis, clone NT2RP3000880.
Homo sapiens (Human)
                                                                                                                                                                                                 33 AA.
                                 2; Mismatches
                  Pred. No. 25;
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                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95127729; PubMed=7827104;
                66.78;
                Best Local Similarity 66.7
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                                                                                                                                                                                                                                                                                                                                       Mammalia, Butheria, Ceta.
Bovidae, Caprinae, Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                       165 CYDLQRNDMRKI 176
                                                                     1 CFOLORN-MRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQLQRNMRKV 11
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Query Match
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Query Match

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Gaps

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Indels

Length 573;

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"Urease operon of Lactobacillus fermentum,";
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: UREA + H(2)O = CO(2) + 2 NH(3).
-!- COFACTOR: EACH CHAIN BINDS TWO NICKEL IONS (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE UREASE FAMILY.
EMBL; AF120718; AAD22480.1; --
HSSP; P41020; 1UBP.
                                                                                                                                                                                                                                                                                                                 InterPro; IPR01924; UreaseA.
Pfam; PF00449; urease, 1.
Pfam; PF00449; urease C; 1.
PROSITE; PS01120; UREASE 1; 1.
PROSITE; PS01120; UREASE 2; 1.
Hydrolase; Metal-binding; Nickel.
SEQUENCE 573 AA; 61823 MW; 4D325C6C4A21559C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.4%; Score 38; DB 2; 58.3%; Pred. No. 39; iive 2; Mismatches
                                                                Coton E., Visser J.J., Van Vuuren H.J.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQLQRNMRKVR 12
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Best Local Similarity
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01-MAR-2002
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Q9UUT7
AC Q9UUT
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DE Subun
DE Drecu
GN NUKM.
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Rhabditidae; Peloderinae, Caenorhabditis.
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lactobacillus fermentum.
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Lactobacillaceae; Lactobacillus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nateration R.;

Nateration R.;

Nateration R.;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

E Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

InterPro; IRR0010163; 7TM chemol.

R InterPro; IRR001058; 7TM nematode.

InterPro; IRR001058; 7TM nematode.

InterPro; IRR001058; 7TM nematode.

R Pfam; PF01461; 7TM 4; 1.

R ProsITE; PS00030; RRM_RNP_1; UNKNOWN_1.

W Hypothetical protein.

SEQUENCE 335 AA; 38704 MW; 04A8CEE6CDB8C5F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 335;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Du Z., Maggi L.;
"The sequence of C. elegans cosmid K10C9.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNA-2002 (TrEMBLrel. 21, Last amnotation update)
Urease (EC 3.5.1.5) (Urea amidohydrolase).
                                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 38.7 kDa protein.
                                     2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          573 A.A.
                                                                                                                                                                                                                                                                                                                                  335 AA.
      Pred. No. 8.6;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99069613; PubMed=9851916;
60.08;
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                                        6; Conservative
                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
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      Best Local Similarity
                                                                                                  1 CFQLQRNMRK 10
                                                                                                                                                               70 CFSLOONFKK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09S6F6;
                                                                                                                                                                                                                                                                                                                                                                061888;
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                                            Matches
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061888
10061888
101-001-A
DT 01-7
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01-MAY.2000 (TrEMBLrel. 13, Last sequence update)
01-MAR.2002 (TrEMBLrel. 20, Last annotation update)
Subunit NUKM of protein NADH:ubiquinone oxidoreductase (Complex I)
Precursor (EC 1.6.99.3).
NUKM.
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=2195285; PubMed=11759840; Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Wataneko T., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara W., Matsumoto M., Matsumo A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.; Sugimoto of the filamentous nitrogen-fixing cyanobacterium Anabaena sp. strain PCC 7120."; DNA Res. 8:205-213(2001).
BMBL; AP003892; BAB724391; Complete protecome. SEQUENCE 187 AA; 21356 MW; 85C13C2EC8831DA9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                      Bacteria; Čyanobacteria; Nostocales; Nostocaceae; Nostoc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Indels
01-WAR-2002 (TrEMBLrel. 20, Created)
01-WAR-2002 (TrEMBLrel. 20, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
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SEQUENCE FROM N.A.

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SCHWARTZ J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Vysotskaia V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
Lee J., Liu A., Li J., Kremenetskaia I., Gonzalez A., Altafi H.,
A Araujo R., Brooks S., Buehler E., Chao O., Conn L., Conway A.B.,
Dunn P., Hansen N., Huizar L., Khan S., Kim C., Palm C., Rowley D.,
Shinn P., Walker M., Davis R.W., Ecker J.R., Federspiel N.A.,
A Theologis A.,
"Arabidopsis thaliana chromosome 1 BAC F16N3 sequence.",
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.

EMBL, AC007519; AAD46030.1; -
REMBL, AC007519; AAD46030.1; -
REMBL, AC007518; Fahnd.

REMBL, AC007518; FF HAND; UNKNOWN 1.

REMSLYEL SEQUENCE 887 AA, 99221 MW; CEC76948485882E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta, Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                       Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A., Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.; "Complete genome sequence of Clostridium perfringens, an anaerobic
                                                                                                                               Clostridium perfringens.
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.8%; Score 37; DB 16; Length 565; 70.0%; Pred. No. 60; 2; Indels tive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRFAMS; TIGRO0456; argS; 1.
PROSITE; PS00178; AA TRNA LIGASE I; 1.
PROSITE; PS00307; LECTIN LEGUME BETA; UNKNOWN 1.
Ligase; Complete proteome.
SEQUENCE 565 AA; 64626 MW; 2626BD869B6ED66E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNI-2001 (TrEMBLrel. 17, Last annotation update)
F16N3.17 protein.
                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                             flesh_eater.";
Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
EMBL; AP03131; BAB81367.1;
InterPro; IPR001278; Arg tRNA-synt_1c.
InterPro; IPR01220; Lectin_legB.
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                                         Created)
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   PRT;
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InterPro, IPR001412; tRNA-synt_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF03485; N-Arg; 1.
Pfam; PF00750; tRNA-synt 1d; 1.
PRINTS; PR01038; TRNASXNTHARG.
                                     01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-JUN-2002 (TrEMBLrel. 21,
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Query Motch
Best Local Similarity 70.00,
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   PRELIMINARY;
                                                                                             Arginine-tRNA ligase.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=13 / TYPE A;
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                                                                                                                                                                                         NCBI_TaxID=1502;
                                                                                                                                                                                                                                                                     PubMed=11792842;
                                                                                                                   ARGS OR CPE1661,
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                                                                                                             STRAIN=E 150;
MEDLINB=20439569; PubMed=10924914;
MEDLINB=20439569; PubMed=10924914;
Lindall M., Schaegger H., Kerscher S., Zwicker K., Radermacher M.,
Lindall M., Schaegger H., Brandt U.;
"Biophysical and structural characterization of proton-translocating
NADH-Dehydrogenase (complex I) from the strictly aerobic yeast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT NUKM OF PROTEIN NADH:UBIQUINONE OXIDOREDUCTASE (COMPLEX 1).
C976335ECFD686ED CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Yarrowia lipolytica (Candida lipolytica).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Dipodascaceae, Yarrowia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.8%; Score 37; DB 3; Length 210; 63.6%; Pred. No. 23; tive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AMEM.; PF02117; Sra; 1.
PFGUENCE 346 AA; 40696 MW; SEA98035D4E93B5B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                       346 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81484; CAB03971.1; -
InterPro; IPR000344; Sra_chemo_Ce.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                           210 AA; 23430 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-1998 (TrEMBLrel. 06, 01-JUN-1998 (TrEMBLrel. 06, 01-MAR-2002 (TrEMBLrel. 20,
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les 6; Conservative
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230 YQLEANMRNIR 240
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Best Local Similarity
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                                                                                           SEQUENCE FROM N.A.
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                                                   NCBI_TaxID=4952;
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SEQUENCE

Matches

Basham V.M.;

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C47A10.6

045308; 045308

RESULT 13

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Query Match

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RESULT 14

Q8XJU2

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Gaps

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Query Match
Best Local Similarity 50.0%; Pred. No. 94;
Matches 6; Conservative 3; Mismatches 3; Indels
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OY 1 CFOLORNWEKVR 12 | | :::| | | | | bb 659 CHOIEKNERNVR 670

Search completed: February 21, 2003, 07:44:35 Job time : 22.8 secs

us-09-743-107b-81.rag

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Human lactoferrin
Human lactoferrin
Human lactoferrin
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                                                                                                                                                                   February 21, 2003, 07:25:55 ; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
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1: /SIDS2/gcgdata/geneseq/geneseqp.embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseqg.embl/AA41981.DAT:*
3: /SIDS2/gcgdata/geneseqg.embl/AA41981.DAT:*
4: /SIDS2/gcgdata/geneseqg.embl/AA41981.DAT:*
5: /SIDS2/gcgdata/geneseqg.embl/AA41981.DAT:*
6: /SIDS2/gcgdata/geneseqg.embl/AA41984.DAT:*
7: /SIDS2/gcgdata/geneseqg.embl/AA41986.DAT:*
8: /SIDS2/gcgdata/geneseqg.embl/AA41986.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              908470 segs, 133250620 residues
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Maximum Match 100%
Listing first 45 summaries
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AAY78050
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AAY78037
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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ALIGNMENTS

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Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumou
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                    Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                    Human lactoferrin derived peptide SEQ ID NO:81.
                  AAY78081 standard; Peptide; 12 AA
                                                                                                                                                                                                                                                                  98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                               25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                (ASCI-) A+ SCI INVEST AB.
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                                                                                                                                                                 Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                              06-JUL-1999;
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29-DEC-1998;
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                                          AAY78081;
RESULT 1
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anti-tumour;

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hary 8001 to hary 8100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colltis; Candida infection; fungicidal;
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            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                Claim 22; Page 36; 102pp; English
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98SE-0002562.
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AAY78001 to AAY78100 represent peptides having sequences based on human

Claim 12; Page 70; 102pp; English.

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        hadrontian. The peptides are cased up to the intercine currolled through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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lactoferrin. The peptides are taken up in the intestine through
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98SE-0002562.
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                           12 AA;
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us-09-743-107b-81.rag

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                   Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative
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fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                                                      Length 12;
                                                                                                                                                                    Score 68; DB 21; Length 14, Pred. No. 7.4e-05;
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98SE-0002562.
98SE-0004614.
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Best Local Similarity
Matches 11; Conserv
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17-JUL-1998;
29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through the opecific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as universet infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also are though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis based on lactoferrin would costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
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                 Length 12;
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Pred. No. 8e-05;
1; Mismatches 0; Indels
Score 68; DB 21; Lengtu ....
Pred. No. 7.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dolphin GT;
                                                                                                                                                                                                                                                                                                      Human lactoferrin derived peptide SEQ ID NO:37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 70; 102pp; English.
                                                                                                                                                                                                  AAY78037 standard; Peptide; 13
               95.8%;
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                                                  11; Conservative
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                  12
                                                                                                     1 CFOWORNMRKVR 12
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                                 Local Similarity
                                                                                  1 CFQWQKNMRKVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200001730-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                   AAY78037;
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               Query Match
                                               Matches
                                                                                                                                                                                      AAY78037
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us-09-743-107b-81.rag

Human lactoferrin derived peptide SEQ ID NO:49.

(first entry)

25-APR-2000

AAY78049 standard; Peptide; 13 AA

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the directlation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower.
                                                                                                                                                                                                                                                                   Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
unrinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 21; Length 13;
Pred. No. 8e-05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                          AAY78048 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 15; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mattsby-Baltzer I,
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91.7%;
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98SE-0002562.
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                                                                                                                                                                                                (first entry)
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Best Local Similarity 91.7
Matches 11; Conservative
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1 CFOWOKNMRKVR 12
                   2 CFQWQRNMRKVR 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on human
                                                                                                                     Human, lactoferrin, modification, infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urlnary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 74; 102pp; English.
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Best Local Similarity
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                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                              06-JUL-1999;
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CFQWQKNMRKVR 12 CFQWQRNMRKVR 13

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RESULT 7 AAY78049

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Synthetic.

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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
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                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                        Claim 12; Page 69; 102pp; English.
                                                                                                                                             98SE-0002441.
                                                                                                                                                       98SE-0002562.
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                                                                                                                          99WO-SE01230.
                                      bactericidal; preservative.
                                                                                                                                                                                  (ASCI-) A+ SCI INVEST AB.
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                                                                                    WO200001730-A1.
                                                         Homo sapiens.
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                                                                   Synthetic.
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. AAY78001 to AAY78100 represent peptides having sequences based on human Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

95.8%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 8.6e-05; ive 1; Mismatches 0; Indels 11; Conservative Best Local Similarity 14 AA; Sequence Query Match Matches ð

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Gaps . 0

AAY78050 standard; Peptide; 14 AA. AAY78050; RESULT 9 **AAY**78050

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colliis; Candida infection; fungicidal;

bactericidal; preservative.

Homo sapiens.

Synthetic.

99WO-SE01230.

06-JUL-1999;

13-JAN-2000.

WO200001730-A1.

Human lactoferrin derived peptide SEQ ID NO:51.

Human lactoferrin derived peptide SEQ ID NO:50.

(first entry)

25-APR-2000

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; pactericidal; preservative

Homo sapiens

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lactoferin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a wucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                        Dolphin GT;
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                                                                                                                                                                                                                                                                                                           Claim 15; Page 75; 102pp; English.
                                                                                                                 98SE-0002441.
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                                                                                    99WO-SE01230
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                                                                                    06-JUL-1999;
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Pred. No. 8.6e-05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                     Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 18; Page 75; 102pp; English
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                                                                                                                                                                                                                     Hanson LA, Mattsby-Baltzer I,
                          98SE-0002441.
98SE-0002562.
98SE-0004614.
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Best Local Similarity 91.7"
                                                                                                                                                      (ASCI-) A+ SCI INVEST AB.
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               The agent is low
                               It can be
                                                                                                                                                                                                                                                                                                                                                                                                                             Human, lactoferrin, modification, infection, inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial, anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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            AAR99531-54 are peptides used in an anti-ulcer agent. The ax
in toxicity, is heat-resistant and stable in aqueous soln..
administered orally and be produced in large amounts.
                                                                                                             Score 68; DB 17; Length 15; Pred. No. 9.2e-05; 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 69; 102pp; English.
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                                                                                                                 95.8%;
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98SE-0004614
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                                                                                                                                                11; Conservative
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                                                                                                                 Query Match
Best Local Similarity
                                                                                  15 AA;
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29-DEC-1998;
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AAY78063 standard; Peptide; 15 AA.

RESULT 14

AAY78063 ID AAY7

25-APR-2000 (first entry)

AAY78063;

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                                                                                                                                                                                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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 Length 15;
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Score 68; DB 21; Length 15
Pred. No. 9.2e-05;
1; Mismatches 0; Indels
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95.8%;
91.7%;
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            Best Local Similarity
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29-DEC-1998;
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Best Local S
Query Match
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                                                                                                  Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection, fungicidal;
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                                                                   Human lactoferrin derived peptide SEQ ID NO:63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 81; 102pp; English.
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                                                                                                                                                       bactericidal; preservative.
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Best Local Similarity
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an infant and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
                                                                                              Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                          Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 68; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                              98SE-0002441.
98SE-0002562.
98SE-0004614.
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17-JUL-1998;
29-DEC-1998;
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                                                                                                                                                                                                    Homo sapiens
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0; Gaps 95.8%; Score 68; DB 21; Length 16; 91.7%; Pred. No. 9.8e-05; ive 1; Mismatches 0; Indels Best Local Similarity 91.7 Matches 11; Conservative Query Match à

16 AA;

Sequence

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1 CFQWQKNMRKVR 12

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2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
6: /cgn2_6/prodata/1/iaa/PCTUS COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-08-455-948-8

US-08-475-055-8

US-08-475-055-8

US-08-204-487-1

US-08-204-487-1

US-08-204-487-1

US-08-204-487-1

US-08-21-174-3

US-08-21-174-3

US-08-21-174-1

US-08-21-174-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-08-256-771-30

US-08-464-1828-6

US-08-464-1828-6

US-08-464-1828-6

US-08-464-1828-6

US-08-464-1828-6

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US-08-464-1828-6

US-08-464-1828-6
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                 OM protein - protein search, using sw model
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seq length: 2000000000
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Match Length DB
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Maximum DB
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Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MATARI, HIDEKI
APPLICANT: TANARA, SHICERALI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INMIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/204,487
FILING DATE: 02-MAR.1994
CLASSIFICATION: 514
US-08-464-182h-2
US-08-74-586-2
US-08-724-586-2
US-08-421-632-2
US-08-655-640-2
US-08-655-640-4
US-08-154-019-4
US-08-161-33-4
US-08-161-33-4
US-08-161-33-4
US-08-161-33-4
US-08-161-33-4
US-08-158-31-3
US-08-158-31-3
US-08-456-106-2
US-08-456-106-2
US-08-456-106-2
US-08-456-106-2
US-08-456-106-2
US-08-456-108-2
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NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCS/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELEPAX: (617) 248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18 amino acids
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MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 18 amino TYPE: amino acid
       STRANDEDNESS:
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us-09-743-107b-81.rai

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18 amino acids
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                               STATE: New Jersey COUNTRY: USA
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Best Local Similarity
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US-08-628-380-8
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                                                                      US-08-628-380-8
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Patent No. 585882
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: YOUG MING LI
APPLICANT: ANTHONY CERANT
TITLE OF INVENTION: ADENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                      Length 18;
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                                                                  Query Match 95.8%; Score 68; DB 1; Length 18; Best Local Similarity 91.7%; Pred. No. 4.5e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 2; I
Pred. No. 4.5e-05;
1; Mismatches 0;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
FILING DATE: ARRIL 7, 1995
FILING DATE: ARRIL 7, 1995
CLASSIFICATION NUMBER: 08/418,642
FILING DATE: ARRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,747-1-00
TELEFRONCE/DOCKET NUMBER: 26,747-1-00
TELEFRONCE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 411 Hackensack Avenue
CITY: Hackensack
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US-08-204-487-3
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INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 91.7%;
Matches 11; Conservative
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DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
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; FRAGMENT TYPE: internal
US-08-485-948-8
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
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0;
Patent No. 5891341

GENERAL INFORMATION:

RAPLICANT: LI, YONG MING

APPLICANT: CERAMI, ANTHONY

TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS

NUMBER OF SEQUENCES:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 4

18-08-475-055-8

18-08-475-055-8

18-08-475-055

19 Patent No. 5962245

19 GENERAL INFORMATION:

APPLICANT: HELEN VLASSARA

APPLICANT: HELEN VLASSARA

APPLICANT: ANTHONY CERAMI

TITLE OF INVENTION: ARGENTE FOR BINDING TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: BNDPRODUCTS, AND METHODS OF THEIR USE

NUMBER OF SEQUENCES: 9
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                                                                                                                                                                                                                                                                                                                                                         ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLORABLICATION 314
PLIASSIFICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRLI 7, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REPRENCE/DOCKET NUMBER: 947-1-008 CIP
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1949-5800
TELECATION TO 1849-1684
TELEX: 133521
INFORMATION FOR ESQ. ID NO: 8:
                                                                                                                                                                                                                                                          : 411 Hackensack Avenue
Hackensack
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OPERATING SYSTEM: MS-DOS
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TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL LINE:
ORGANELLE:
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APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                 COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 2; I Pred. No. 4.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.8%; Scor.
91.7%; Pred. No. *.-
1; Mismatches
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MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/488,217
FILING DATE: UNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: UNE 7, 1995
CLASSIFICATION NUMBER: 08/418,642
FILING DATE: TOPER 7, 1995
CLASSIFICATION: NUMBER: 20,742
REGISTRATION NUMBER: 26,742
REFRENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/07755161A Patent No. 5304633
                ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 133521
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acids STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
CORRESPONDENCE ADDRESS:
                                                                     STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWOKNMRKVR 12
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COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; FRAGMENT TYPE:
US-08-475-055-8
                                                                                    COUNTRY: U
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US-07-755-161A-3
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: O'S residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" FUBLICATION INFORMATION:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
FILING DATE:
RUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                           FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN W. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
FRATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                               TELEPHONE: 202-371-885
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 19
IDENTIFICATION METHOD:
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DEVELOPMENTAL STAGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
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95.8%; Score 68; DB 1; Length 20;

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FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 91.77
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                   DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 02109
                                                                                                                                                                                                                                                                        TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: M
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                                     0;
Pred. No. 5e-05;
                                                                                                                                                    RESULT 6
US-07-891-174-3
Sequence 3, Application US/07891174
Setent No. 5317084
Patent No. 5317084
TITLE OF INVENTION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCHWARE: Displaywrice
CURRENT APPLICATION DATA:
APPLICATION NDTAE:
TLING DATE: 29-MAY-1992
CLASSIFICATION DATA:
APPLICATION NAME: 30
RIOR APPLICATION DATE:
APPLICATION DATE: 05-SEP-1991
FILING DATE: 05-SEP-1991
ATTORNEY AGENT INFORMATION:
NAME: WATERN M. Cheek Jr.
REGISTRATION NUMBER: 33-367
REGISTRATION NUMBER: 33-367
REGISTRATION NUMBER: 33-367
REPERBUNE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION 18956
               Best Local Similarity 91.7%;
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NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                               11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
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DEVELOPMENTAL STAGE:
                                                                                    2 CFQWQRNMRKVR 13
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CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                   1 CFQWQKNMRKVR 12
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBERRY:
CLONE:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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MOLECULE TYPE:
HYPOTHETICAL:
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TISSUE TYPE:
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                                 Matches
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IDBNTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: /note= "thiol group of Cys residue at location 19" |
FEATURE: NAME/KEY: modified site | LOCATION: 19 |
IDBNTIFICATION METHOD: | IDBNTIFICATION METHOD: | IDBNTIFICATION | OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: /note= "thiol group of Cys residue at location 2" |
OTHER INFORMATION: /hold group of Cys residue at location 2" |
ANTHORS: ANTHORS: ANTHORS: ANTHORS: ANTHORS: ANTHORS: | ANTHORS: |
ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | ANTHORS: | AN
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APPLICANT: NAKABILMA, HIDEKI
APPLICANT: NAKABILMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICBRALI
APPLICANT: TANAKA, SHICBRALI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: UNUBLIDA, TOSHIAKI
TITLE OF INVENTION: UNRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSE: THIBEAULT
STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 20;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB 1;
Pred. No. 5e-05;
1; Mismatches
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NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
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US-08-256-771-24
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US-08-381-984-24
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Patent No. 5656591

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: AMTIMICROBIAL AGENTS AND METHOD FOR TREATING TITLE OF INVENTION: PRODUCTS THEREMITH NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                           Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 5e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cyg residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US/08/256,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                           1 CFOWOKNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Mac.
STATE: D.C.
COUNTRY: U.S.A.
"TD: 20005
                                                                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
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                                               Gaps
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                                                                                                                                                                                                                               Sequence 25, Application US/08256771
Patent No. 565591
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
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| OTHER INFORMATION: /note= "Cys residues are protected to
| OTHER INFORMATION: prevent disulfide bond"
| US-08-256-771-25
95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 5e-05; 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 5e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IN COMPATIBLE
COMPUTER: MS-DOS
SOFRATING SYSTEM: MS-DOS
SOFRATING SYSTEM: MS-DOS
SOFRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
Query Match
Best Local Similarity 91.77
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                   1 CFOWOKNMRKVR 12
                                                                                                            2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: ...
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWOKNMRKVR 12
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                                                                                                                                                                                           RESULT 9
US-08-256-771-25
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OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment therec
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Patent No. 6423509

GENERAL INFORMATION:

APPLICANT: Samyang Genex Corporation

TITLE OF INVENTION: Wass production method of lactoferrin polypeptide from yeast and

TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION: useful microorganism thereof

TITLE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: LBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER:
  805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                   ATTONEX/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGIESTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 12
SOFTWARE: KOPATENTIN 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQKNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CFOWORNMRKVR 13
                      Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                  U.S.A.
                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                    20005
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NAME/KEY:
                                           STATE: I
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US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 5e-05; Uive 1; Mismatches 0; Indels
             GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIOXIDANT

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IDBN Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
UMMERE OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
Sequence 24, Application US/08381984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEPAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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APPLICATION NUMBER:
FILING DATE:
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LOCATION:
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQKNMRKVR 12
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                                                                                                                                                                                                        D.C.
U.S.A.
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STRANDEDNESS: sin
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LOCATION: 21

DENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
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95.8%; Score 68; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 6.3e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
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PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:

US-07-755-161A-10
                                                              33,367
                                                                                                      TELECOMMUNICATION INFORMATION:
TELEFHONE: 202-371-8850
TELEFAX: 202-371-8856
TELEX:
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
                                        NAME: Warren M. Cheek Jr. REGISTRATION NUMBER: 33,3 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                          SEQUENCE CHARACTER.STICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
  FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: modified site LOCATION: 4 IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQKNIMRKVR 12
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CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
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ISSUE:
PAGES:
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                  Sequence 6, Application US/09508734
Patent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
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                                                                                                                                                     Gaps
                                                                                                                                                     .;
0
                                                                                                    95.8%; Score 68; DB 4; Length 22; 91.7%; Pred. No. 5.5e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95.8%; Score 68; DB 4; Length 24; 91.7%; Pred. No. 6e-05;
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Sequence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
CORRESPONDENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITT. Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TILE REPERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR PILING DATE: 1999-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR FILING DATE: 1998-07-13
SOFTWARE: Kopatentin 1.71
SOFTWARE: Kopatentin 1.71
TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                          Best Local Similarity 91.73
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                           1 CFQWQKNMRKVR 12
                                                                                                                                                                                                                   2 CFQWQRNMRKVR 13
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                                                                                                                                                                                                                                                                                                                 US-09-508-734-6
                                                              US-09-508-734-4
LENGTH: 22
                                                                                                        Query Match
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Search completed: February 21, 2003, 07:50:36 Job time : 9.7 secs
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PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER:
                                                                                                                                                                                                                                                              JOURNAL:
                                                                                                                                                                                     AUTHORS:
                                                                                                                                                                                                                                                                                             VOLUME:
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LICRATION HETHOD:

DENTIFICATION METHOD:

OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                         Sequence 10, Application US/07891174

| Patent No. 5317084
| GENERAL INFORMATION:
| APPLICAMT Mamoru TOMITA et al. TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
| CORRESPONDENCE ADDRESS: ADDRESSE: ADDRESSE: Monderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STREET: U.S.A.
| COUNTRY: U.S.A. ZIP: 20005
| COUNTRY: Exabale FORM: MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible CORPUTER: IBM COMPATER: Diskette, 5.25 inch, 500Kb CORPUTER: IBM COMPATER: DISKETER: DISKETER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: Modified site
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21
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
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STRAIN:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
RESULT 15
US-07-891-174-10
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" PUBLICATION INFORMATION:
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95.8%; Score 68; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 6.3e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
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GenCore version 5.1 3
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February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec Published Applications AA:*

1: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(NEW \) PUB. pep: *

2: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(NEW \) PUB. pep: *

3: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(NEW \) PUB. pep: *

4: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(NEW \) PUB. pep: *

5: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(NEW \) PUB. pep: *

6: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(PUBCOMB. pep: *

7: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(PUBCOMB. pep: *

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9: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(PUBCOMB. pep: *

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10: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(PUBCOMB. pep: *

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12: \(cgn2_6 \) prodata/2 \) pubpaa/USOB \(PUBCOMB. pep: *

13: \(cgn2_6 \) prodata/2 \) pubpaa/USSOB \(PUBCOMB. pep: *

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14: \(cgn2_6 \) prodata/2 \) pubpaa/USSOB \(PUBCOMB. pep: *

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14: \(cgn2_6 \) prodata/2 \) pubpaa/USSOB \(PUBCOMB. pep: *

14: \(cgn2_6 \) prodata/2 \) pubpaa/USSOB \(PUBCOMB. pep: * 156504 GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd. Total number of hits satisfying chosen parameters: 156504 seqs, 31069816 residues Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries OM protein - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 200000000 US-09-743-107B-81 71 1 CFQWQKNMRKVR 12 Perfect score: Scoring table: Database : Sequence: Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Segmence 2. Appli	Semiland 00 appendix			· ~		. 4	4	000		Ö	000	Sequence 46393. A	Sequence 58. Appl	8	Semence 58. April	0 0	,	sednence 4T00Z, A	Sequence 37353, A
ΠD	US-09-798-869-2	US-09-798-869-20	US-10-023-096-2	US-09-798-869-6	US-09-798-869-3	US-09-798-869-23	LS-09-198-869-7	US-09-798-869-4	US-09-798-869-22	US-09-798-869-8	US-09-798-869-29	US-09-798-869-30	US-09-864-761-46393	US-10-066-500-58	US-10-002-796-58	US-10-066-273-58	US-10-066-494-58	110-09-064-751-41000	70074-70/-400-60-00	US-09-864-761-37353
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Query Match	95.8	95.8	95.8	88.7	71.8	71.8	64.8	63.4	63.4	59.2	59.5	59.2	52.1	52.1	52.1	52.1	52.1	70	1	20.7
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US-0 US-0 US-0	US-09-864-761-47 US-09-864-761-44 US-09-815-242-12 US-09-815-242-13	US-09-853-625B-16 US-10-081-309-2 US-10-133-912-18 US-10-133-912-19	US-09-265-606-2 US-10-001-189-60 US-10-028-072-38 US-10-121-049-38	US-10-123-904-38 US-10-140-470-38 US-10-175-746-38 US-10-176-918-38 US-10-176-921-38	US-10-137-865-38 US-10-140-474-38 US-09-995-542-12 US-09-995-542-10 US-09-997-641-2
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ALIGNMENTS

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Gaps
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                                                                                      APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: HALDUR SVENDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASEURD for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
APPLICANT: OTHN SIGHEN SVENDSEN
APPLICANT: (YSTEIN REKAAL); APPLICANT: BALDUR SVEINBJ(RNSSON)
                          ; Sequence 2, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.77
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3 CFOWORNWRKVR 14
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US-09-798-869-2
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ORGANISM: Artificial Sequence
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               Best Local Similarity
Matches 11; Conserva
                                                                                    1 CFOWOKNMRKVR 12
                                                                                                           22 CFQWQRNMRKVR 33
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TYPE: PRT
ORGANISM: CAPRINE
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JS-09-798-869-3
                                                                                                                                                                                        RESULT 4
US-09-798-869-6
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Query Match
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APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                                                                                   Query Match 95.8%; Score 68; DB 9; Length 25; Best Local Similarity 91.7%; Pred. No. 4.6e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
         FILE REFERENCE: A34049-PCT-USA-A
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SED ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10505/P58185C
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CLASETPICATION:
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/10023096
Patent No. US20020160941A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Player, William E.
REGIETRATION UNUMBER: 31,409
REFERENCE/DOCKET NUMBER: 1050:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639-6666
TELEPAK: (202) 339-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    , MOLECULE TYPE: protein US-10-023-096-2
LARS VORLAND
                                                                                                                                                                                                                                                                            TYPE: PRT
CRGANISM: Homo Sapiens
US-09-798-869-20
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| Query Match | 95.84; Score 60; DB 9; Length 694; |
| Aktchee | 11; | Conservative | 1; | Mismatchee | 10; | Indels | 0; | Gaps | 0; |
| Aktchee | 11; | Conservative | 1; | Mismatchee | 10; | Indels | 0; | Conservative | 1; | Mismatchee | 0; | Indels | 0; | Conservative | 1; | Mismatchee | 1; | Conservative | 1; | Mismatchee | 0; | Indels | 0; | Conservative | 1; | Mismatchee | 1; | Conservative | 1; | Mismatchee | 0; | Indels | 0; | Conservative | 1; | Mismatchee | 1; | 1; | Mismatchee
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Indels

3; Mismatches

7; Conservative

Matches

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Gaps
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                                                                                                                                                                                                            APPLICANT: (YSTEIN REXDAL
APPLICANT: (YSTEIN REXDAL
APPLICANT: (YSTEIN REXDAL
APPLICANT: BALDON SVEENBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02651
PRIOR APPLICATION NUMBER: PCT/GB99/02651
PRIOR APPLICATION NUMBER: CT/GB99/02651
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 22, Application US/09798869
Publication No. US20030022821A1
GERERAL INFORMATION:
APPLICANT: UCHN SIGURD SVENDSEN
APPLICANT: UCHN SIGURD SVENDSEN
APPLICANT: LARS VORLAND
ITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: AJ4049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-7
RIOR APPLICATION NUMBER: CTT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAISEQ for Windows Version 4.0
SEQ ID NO 25
                                                                                                                                                       ; Sequence 4, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 63.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7; Conservative
    1 CFQWQKNMRKV 11
                                3 CYQWQWRMRKL 13
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Matches 7; Conserv
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ORGANISM: MURINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-09-798-869-22
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Gaps
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US-09-798-869-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:

APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEN REKALL
APPLICANT: GYSTEN REKALL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
FILE REFERENCE: 1990-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PSELSEQ for Windows Version 4.0
SCATURNET 25
                                                                                                                                                                                   ; Sequence 23, Application US/09798869; Publication No. US20030022821A1
GENERAL INFORMATION: APPLICANT: JOHN SIGHRD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 7, Application US/09798869; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                        APPLICANT: (YSTEIN REKCAL
APPLICANT: BALDUR SVEINBU (RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                  1 CFOWOKNIMIRKV 11
                                                           3 CYQWQRRMRKL 13
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ORGANISM: CAPRINE
                                                                                                                                         RESULT 6
US-09-798-869-23
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LENGTH: 15
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US-09-798-869-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.2%; Score 42; DB 9; Length 15; 63.6%; Pred. No. 0.48; artive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 29, Application US/09798869
; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
APPLICANT: JOHN SIGHED SYENDERN
; APPLICANT: (YSTEIN REKDAL
; APPLICANT: LARS WORLAND
; TITLE REFERENCE: A34049-FOT-USA-A
; CURRENT APPLICATION NUMBER: US/09/798,869
; CURRENT FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR APPLICATION NUMBER: GB9818938.4
; PRIOR SEQ ID NOS: 30
; SOFTWARE: FastESQ for Windows Version 4.0
; SEQ ID NO 29
                                                                                                                                                                                               FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
FRIOR RELING DATE: 1999-08-31
PRIOR RELING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PRECEEQ for Windows Version 4.0
SERIOTH: 15
                                        Sequence 8, Application US/09798869
Publication No. US2030022821A1
PUBLICATION:
APPLICANT: JOHN SIGURD SVENDEN
APPLICANT: RYSTEIN REKDAL
APPLICANT: BALDUR SVENDAL
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity
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ORGANISM: BOVINE
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RESULT 10
US-09-798-869-8
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APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Wensheng
TITLE BETERRANGE, Lowid K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REPERRENCE: Acountca-X-1
CURRENT APPLICATION WHERE: US 60/180,312
PRIOR APPLICATION WHERE: US 60/207,456
PRIOR FILING DATE: 2000-00-23
PRIOR PELING DATE: 2000-00-03
PRIOR FILING DATE: 2000-00-03
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
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Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OTHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: LAKE VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9918938.4
PRIOR APPLICATION NUMBER: GB9918938.4
PRIOR APPLICATION NUMBER: GB9918938.4
PRIOR PRIUNG DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQUENCE: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 46393, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
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Best Local Similarity 54.5
Matches 6; Conservative
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ORGANISM: BOVINE
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RESULT 12 US-09-798-869-30

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CURRENT APPLICATION WUMBER: US/10/066,500
CURRENT PAPLICATION NUMBER: 10/002,796
PRIOR PLING DATE: 2002-01
PRIOR APPLICATION NUMBER: 10/002,796
PRIOR PLING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/056974
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.3
OTHER INFORMATION: EST_HUMAN HIT: N80993.1, EVALUE 9.00e-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PELING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILICATION NUMBER: US 09/608,408
PRIOR PILICATION NUMBER: US 09/774,203
PRIOR APPLICATION NUMBER: US 09/774,2
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OTHER INFORMATION: MAP TO ACO18719.2
OTHER INFORMATION: EXPRESSED IN BRAIN
OTHER INFORMATION: EXPRESSED IN ADUL!
OTHER INFORMATION: EXPRESSED IN ADUL!
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Patent No. US20020177165A1
GENERAL INFORMATION:
APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: Luc Desnoyers
APPLICANT: Luc Desnoyers
APPLICANT: David A. Bottein
APPLICANT: Napoleone Ferrara
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Hanspeter Gerber
Mary E. Gerritsen
Audrey Goddard
Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
FILING DATE: 2001-01-30
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P.Mickey Williams
William I. Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicholas F. Paoni
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                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match.
Best Local Similarity
Matches 6; Conserv
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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/099811
PRIOR FILING DATE: 1936-09-10
PRIOR FILING DATE: 1936-09-10
PRIOR PELING DATE: 1936-09-10
PRIOR PELING DATE: 1936-09-10
PRIOR PILING DATE: 1936-09-17
PRIOR APPLICATION NUMBER: 60/101922
PRIOR PILING DATE: 1998-09-17
PRIOR PILING DATE: 1998-09-24
PRIOR PILING DATE: 1998-10-28
PRIOR PILING DATE: 1998-10-28
PRIOR APPLICATION NUMBER: 60/10304
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-0-28
PRIOR PILING DATE: 1999-0-15
PRIOR PILING DATE: 1999-0-15
PRIOR PILING DATE: 1999-0-15
PRIOR PELING DATE: 1999-0-15
PRIOR PELING DATE: 1999-0-15
PRIOR PELING DATE: 1999-0-15
PRIOR PELING DATE: 1999-0-26
PRIOR PELING DATE: 1999-0-26
PRIOR PILING DATE: 1999-0-26
PRIOR APPLICATION NUMBER: 60/14509
PRIOR PELING DATE: 1999-0-17
PRIOR PILING DATE: 1999-0-26
PRIOR APPLICATION NUMBER: 60/169495
PRIOR PILING DATE: 1999-0-26
                                                                                                                                                                                                                                                                                                                                                                                                                 DR FILING DATE: 1997-10-29
DR APPLICATION NUMBER: 60/066364
DR APPLICATION NUMBER: 60/066840
DR PILING DATE: 1997-11-21
DR APPLICATION NUMBER: 60/066840
DR FILING DATE: 1997-12-16
DR APPLICATION NUMBER: 60/074086
DR FILING DATE: 1998-02-09
DR APPLICATION NUMBER: 60/074092
DR FILING DATE: 1998-02-09
DR FILING DATE: 1998-02-09
DR APPLICATION NUMBER: 60/079294
DR FILING DATE: 1998-02-09
DR APPLICATION NUMBER: 60/079294
DR FILING DATE: 1998-03-25
                                                                                                                                                                                                       R APPLICATION NUMBER: 60/062816
R FILING DATE: 1997-10-24
R PILING DATE: 1997-10-31
R FILING DATE: 1997-10-31
R APPLICATION NUMBER: 60/063329
R FILING DATE: 1997-10-27
FILING DATE: 1997-09-17
APPLICATION WINBER: 60/059263
APPLICATION ADDRES: 1997-09-18
APPLICATION NUMBER: 60/059588
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APPLICATION NUMBER: 60/062285
FILING DATE: 1997-10-17
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APPLICATION NUMBER: 60/095998
FILING DATE: 1998-08-10
APPLICATION NUMBER: 60/097000
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APPLICATION NUMBER: 60/099803
FILING DATE: 1998-09-10
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APPLICATION NUMBER: 60/099601
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APPLICATION NUMBER: 08/960507
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PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: 1998-09-16
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PRIOR APPLICATION NUMBER: PCT/US98/24855 PRIOR FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 09/886342
PRIOR FILING DATE: 2001-06-19
PRIOR APPLICATION NUMBER: PCT/US98/14552
PRIOR FILING DATE: 1998-07-14 PRIOR APPLICATION NUMBER: PCT/US98/18824 PRIOR FILING DATE: 1998-09-10 PRIOR APPLICATION NUMBER: PCT/US98/19093 PRIOR FILING DATE: 1998-09-14 FRIOR APPLICATION NOTICE...

PRIOR FILING DATE: 2001-03-14

PRIOR APPLICATION NUMBER: 09/866028

PRIOR APPLICATION NUMBER: 09/870574

PRIOR APPLICATION NUMBER: 09/870574

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: 09/872035

PRIOR APPLICATION NUMBER: 09/872035 PRIOR FILING DATE: 1998-09-21
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PRIOR FILING DATE: 1998-09-10
PRIOR FILING DATE: 1998-09-10
PRIOR PELING DATE: 1998-09-10
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PRIOR APPLICATION NUMBER: 09/254460
PRIOR PILING DATE: 1999-03-03
PRIOR PILING DATE: 1999-03-05
PRIOR PELING DATE: 1999-03-05
PRIOR APPLICATION NUMBER: 09/28465
PRIOR APPLICATION NUMBER: 09/28465
PRIOR APPLICATION NUMBER: 09/33228
PRIOR APPLICATION NUMBER: 09/33292
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PRIOR PILING DATE: 1999-06-14 R FILING DATE: 1999-11-12

OR APPLICATION NUMBER: 09/522342

OR FILING DATE: 2000-03-09

OR FILING DATE: 2000-04-13

OR APPLICATION NUMBER: 09/64610

OR APPLICATION NUMBER: 09/64610

OR FILING DATE: 2000-09-18 FILING DATE: 2000-09-18
APPLICATION NUMBER: 09/709238
FILING DATE: 2000-11-08
APPLICATION NUMBER: 09/767609
FILING DATE: 2001-01-22 FILING DATE: 2001-01-22 APPLICATION NUMBER: 09/802706 FILING DATE: 2001-03-09 APPLICATION NUMBER: 09/403297 FILING DATE: 1999-10-18 APPLICATION NUMBER: 09/423741 APPLICATION NUMBER: 09/665350 FILING DATE: 2000-09-18 APPLICATION NUMBER: 09/380137 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/380138 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/380139 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/403296 FILING DATE: 1999-10-18 PRIOR FILING DATE: 1999-11-10 PRIOR APPLICATION NUMBER: 09/423844 APPLICATION NUMBER: 09/136828 FILING DATE: 1998-08-19 APPLICATION NUMBER: 09/158342 FILING DATE: 1999-06-14
APPLICATION NUMBER: 09/333077

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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

TITLE OF INVENTION: ACIDS ENCODING THE SAME

CURRENT APPLICATION NUMBER: US/10/002,796

CURRENT FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/05914

PRIOR APPLICATION NUMBER: 60/059263

PRIOR PILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059268

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PRIOR PILING DATE: 1997-09-17

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52.1%; Score 37; DB 9; Length 747
Best Local Similarity 45.5%; Pred. No. 1.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels
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PRIOR FILING DATE: 1998-11-25
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PRIOR PLILNG DATE: 1999-09-01
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PRIOR PLILNG DATE: 1999-09-01
PRIOR PLILNG DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR PLILNG DATE: 1999-09-15
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Daniel Tumas
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P.Mickey Williams
William I. Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
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Dan L. Eaton
Napoleone Ferrara
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Hanspeter Gerber
Mary E. Gerritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nicholas F. Paoni
Margaret Ann Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
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Mary A. Napier
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R FILING DATE: 1998-03-25

R APPLICATION NUMBER: 60/081049

R APPLICATION NUMBER: 60/095998

R FILING DATE: 1998-04-08

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R APPLICATION NUMBER: 60/09000

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R APPLICATION NUMBER: 60/099601
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R APPLICATION NUMBER: 60/139695
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R FILING DATE: 1998-08-19
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APPLICATION NUMBER: 60/063733
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FILING DATE: 1997-11-25
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APPLICATION NUMBER: 60/074092
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/099803
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/099811
FILING DATE: 1998-09-10
APPLICATION NUMBER: 60/063082
               FILING DATE: 1997-10-31
APPLICATION NUMBER: 60/063329
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APPLICATION NUMBER: 60/074086
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FILING DATE: 1998-09-17
APPLICATION NUMBER: 60/101922
FILING DATE: 1998-09-24
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FILING DATE: 1999-08-17
APPLICATION NUMBER: 60/169495
FILING DATE: 1999-12-07
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APPLICATION NUMBER: 09/136828
FILING DATE: 1998-08-19
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FILING DATE: 1999-07-26
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APPLICATION NUMBER: 08/933821
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FILING DATE: 1998-12-08
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FILING DATE: 2001-06-19
APPLICATION NUMBER: PCT/US98/14552
FILING DATE: 1998-07-14
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APPLICATION NUMBER: PCT/US99/12252 APPLICATION NUMBER: PCT/US98/24855 APPLICATION NUMBER: PCT/US98/25190 PRIOR APPLICATION NUMBER: 09/665350
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PRIOR FILING DATE: 2000-10-08
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PRIOR PELING DATE: 1998-09-14 R FILING DATE: 1999-06-14

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R PILING DATE: 1999-06-14

R APPLICATION NUMBER: 09/333075

R FILING DATE: 1999-06-14

R APPLICATION NUMBER: 09/333077

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R APPLICATION NUMBER: 09/33077

R APPLICATION NUMBER: 09/380137

R APPLICATION DATE: 1999-08-25 TILING DATE: 1999-03-03 APPLICATION NUMBER: 09/254460 FILING DATE: 1999-03-09 APPLICATION NUMBER: 09/254465 FILING DATE: 1999-03-05 APPLICATION NUMBER: 09/284663 APPLICATION NUMBER: 09/332928 APPLICATION NUMBER: 09/380138 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/380139 APPLICATION NUMBER: 09/522342 FILING DATE: 2000-03-09 APPLICATION NUMBER: 09/548815 FILING DATE: 2000-04-13 APPLICATION NUMBER: 09/664610 FILING DATE: 1999-10-18 APPLICATION NUMBER: 09/403297 FILING DATE: 1999-10-18 FILING DATE: 1999-08-25 APPLICATION NUMBER: 09/403296 APPLICATION NUMBER: 09/423741 FILING DATE: 1999-11-10 APPLICATION NUMBER: 09/423844 FILING DATE: 1999-11-12 FILING DATE: 2000-09-18 APPLICATION NUMBER: 09/665350 FILING DATE: 1998-12-01 FILING DATE: 1999-06-02 PRIOR PRIOR

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-81 71 1 CFQWQKNMRKVR 12 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ALIGNMENTS

AESOLI L
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lactotransferrin precursor [validated] - human
N;Alternate names: lactoferrin
C; Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
С; Accession: G01394; S11228; Ā45401; S10324; S15853; S20841: S07160; A61169; A31000; S74
R,Cho, Y.
submitted to the EMBL Data Library, March 1994
A;Reference number: G06820
A;Accession: G01394

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA A; Residues: 1-711 < CHO>

A;Cross-references: EWBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237 R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucleic Acids Res. 18, 5288, 1990
A;Title: Complete nucleotide sequence of human mammary gland lactoferrin. A;Reference number: S11228; MUID:90384839; PMID:2402455

A; Molecule type: mRNA A; Residues: 1.148, T',150-422, 'C',424-711 <RBY> A; Cross-references: EMBL:X53961; NID:334415; PIDN:CAA37914.1; PID:334416 A; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T. Mol. Endocrinol. 6, 1969-1981, 1992 A; Title: Differential molecular mechanism of the estrogen action that regulates lactofer: A; Reference number: A45401; MUID:93125571; PMID:1480183

A; Molecule type: DNA A; Residues: 1-15 <TEN>

A; Cross-references: GB: S52659; NID: g263311; PIDN: AAB24877.1; PID: g263312 A; Experimental source: placenta A; Experimental source: placenta A; Experimental source: placenta A; Note: sequence extracted from NCBI backbone (NCBIP:122202) B; Powell, M.J.; Ogden, J.E. Nucleic Acids Res: 18, 4013, 1990 A; Title: Nucleotide sequence of human lactoferrin cDNA. A; Reference number: S10324; MUID: 90326549; PMID: 2374734

A; Molecule type: mRNA A, Accession: S10324

A; Accession: S15853

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 20-31 <ST1>

A; Accession: S20841

A;Residues: 20-28,'X',30-31 <ST2>

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76.1%;
72.7%;
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      Query Match
Best Local Similarity 72.7
Matches 8; Conservative
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nes 7; Conservative
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                                                                                                                                  1 CFOWOKNIMRKV 11
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tes 7; Conserv
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A;Residues: 1-15 <LIU>
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A; Molecule type: mRNA
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A; Residues: 436-487, 74',489-711 <RAD>
A; Residues: 436-487, 74',489-711 <RAD>
A; Residues: 436-487, 74',489-711 <RAD>
A; Cross-references: EMBLAM18642; NID: 9186815; PIDN: AA886665.1; PID: 9386855
B; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyth A; Reference number: A61169; MUID: 91235214; PMID: 1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 20-140,142-169,171-203, 'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A; Note: this is the final paper in a series
R; Houen, G.; Heegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Blochem. 241, 303-308, 1996
A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A; Reference number: S74119; MUID:97054624; PMID:8898921
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F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;527,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Experimental source: normal breast tissue
R,Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Eur. J. Biochem. 145, 659-666, 1984
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C;Date: 14-701-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Gan, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32 1995
A;Title: Isolarion and characterization of sheep lactoferrin, an inhibitor of platelet A;Accession: S52107; MUID:95127729; PMID:7827104
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-933, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
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A;Molecule type: protein
A;Residues: 13 <QIA>
C;Superfamil: transferrin; transferrin repeat homology
C;Keywords: duplication
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C,Superfamily: transferrin; transferrin repeat homology
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Pred. No. 0.00054;
1; Mismatches 0;
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A;Residues: 3-701,'SWKPVN' <PAN>
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: GDB:119368; OMIM:150210
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91.7%;
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Best Local Similarity 91.7<sup>3</sup>
Matches 11, Conservative
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NiAlternate names: lactotransferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41205
C;Accession: A28438; A1205
B;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Tile: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretise features number: A92596; MUID:87280033; PMID:3611056
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C, Superfamily: transferrin; transferrin repeat homology
C, Superfamily: transferrin; glycoprotein
F,359-696/Domain: transferrin repeat homology <TRH2>
F,359-696/Domain: transferrin repeat homology <TRH2>
F,252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A,Residues: 3-707 <PEN>
A,Cross-references: EMBL:J03298
F.Liu, Y., Teng, C.T.
A,Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A,Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb_1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                          Gaps
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C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-707/Product: lactochransferrin #status predicted <MAT>
F;28-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Score 54; DB 2; Length 33; Pred. No. 0.0069; 2; Mismatches 1; Indels
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R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin CDNA:
A;Reference number: UC2323; MUID:94380047; PMID:8093048
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RESULT 5

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Cispecies: Halobacterium sp. NRC-1
Cibate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cipacession: C84325
Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
Cipate: 02-Feb-2001 #sequence_revision 02-Feb-2001
Cipate: 03-Feb-2001 #sequence_revision 02-Feb-2001
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                         R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Tile: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
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A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
C;Genetics:
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A.Residues: 1-275 <WIL>
A.Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
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C;Species: Caenorhabditis elegans
C;Date: i5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
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Pred. No. 14;
0; Mismatches 5; Indels
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A;Molecule type: DNA
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Best Local Similarity 58.3
Matches 7; Conservative
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Best Local Similarity
6; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-511 <PAR>
                                                                                                                                                                                                                                                                                                                     A; Accession: AB0858
A; Status: preliminary
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A;Molecule type: DNA
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C; Accession: AB0858
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A;Gene: STY3070
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J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: 216302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A,Map position: IX
A,IMap position: IX
A,IMILTONS: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3
C; Superfamily: dynein heavy chain, ciliary
C; Reywords: nuclectide binding; P-loop
F;1919-1926/Region: nuclectide-binding motif A (P-loop)
F;2202-2209/Region: nuclectide-binding motif A (P-loop)
F;2530-2537/Region: nuclectide-binding motif A (P-loop)
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C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2;
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                                                                                                                        dynein beta heavy chain - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: T08030
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C'Accession: T19429
R:Lloyd, C.
submitted to the EMBL Data Library, November 1996
A):Reference number: Z19123
A):Reference number: Z19123
A):Accession: T19429
A):Modecule type: DNA
A):Modecule type: DNA
A):Modecule type: DNA
A):Residues: 1-681 < WIL>
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A;Molecule type: DNA
A;Residues: 1-4568 <MIT>
A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
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Pred. No. 39;
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hypothetical protein C24H11.8 - Caenorhabditis elegans

A; Experimental source: clone C24H11

A; Gene: CESP: C24H11.8

A; Map position: 3

Query Match 60.6 Best Local Similarity 70.0 Matches 7; Conservative

AB0858

3; Mismatches

63.4%; 50.0%;

6; Conservative

Query Match Best Local Similarity Matches 6; Conserva

ð a

A; Experimental source: strain 21gr

Genetics:

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phytochrome C - sorghum
C;Species: Sorghum bicolor (sorghum)
C;Species: Sorghum bicolor
C;Date: 20.Sep-1999 #sequence_revision 20-Sep-1999 #text_change 05-May-2000
C;Date: 20.Sep-1999 #text_change 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily: phytochrome; phytochrome homology
C;Keywords: chromoprotein; dimer; photoreceptor; phytochromobilin; transcription regula:
E;65-581/Domain: phytochrome homology <PHY>
F;321/Binding site: phytochromobilin (Cys) (covalent) #status predicted
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A,Residues: 1-1274 <BEV>
A;Cross-references: EMBL:AL049482
A;Experimental source: cultivar Columbia; BAC clone F17A8
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity 60.0
Matches 6; Conservative
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A;Molecule type: DNA
A;Residues: 1-206 <KUR>
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A; Note: F17A8.60
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C.Species: Thermotoga maritima
C.Spate: ll-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C.Accession: D72378
R.Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: D72378
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BNA Res. 8, 205-213, 2001
A; Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A; Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Cross-references: GB:AE001721; GB:AE000512; NID:g4980922; PIDN:AAD35505.1; PID:g498092
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A;Cross-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179
A;Experimental source: strain PCC 7120
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0
A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                           57.7%; Score 41; DB 2; Length 275; 63.6%; Pred. No. 11; 2; Indels ative 2; Mismatches 2; Indels
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Pred. No. 26;
1; Mismatches
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C;Superfamily: maltose transport protein malG
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Best Local Similarity 66.7<sup>3</sup>
Matches 6; Conservative
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A,Cross-references: GB:AE007869; PIDN:AAK86569.1; PID:g15155733; GSPDB:GN00169
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                                                                                                                                                     Query Match
53.5%; Score 38; DB 2; Length 206;
Best Local Similarity 50.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 4; Indels
                          C;Genetics:
A;Gene: AGR C 1381
A;Map position: circular chromosome
C;Superfamily: pyridoxamine-phosphate oxidase
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1 CFOWOKNARKVR 12

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88 CFHWKSLRROVR 99 DP

PASA D. D. Phosphate oxidase [imported] - Agrobacterium tumefaciens (strain C58, Du C; Species: Agrobacterium tumefaciens C; Species: Agrocession: AB2670
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A; Reference number: AB2670
A; Reference number: AB2670
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-206 < XUR>
A; Connected C58.
A; Experimental source: strain C58 (Pupont)

A,Map position: circular chromosome C,Superfamily: pyridoxamine-phosphate oxidase

0; Gaps Query Match
Best Local Similarity 50.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 4; Indels

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1 CFOWOKNMRKVR 12

| | |: |:|| 88 CFHWKSLRRQVR 99

Search completed: February 21, 2003, 07:47:53 Job time: 9.65 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-81 71 1 CFQWQKNMRKVR 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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P14632 sus scrofa 077698 bubalus bub Q00020 broad bean P13217 drosophila Q9xwj9 ryza sativ Q9xmj5 drosophila P23374 bacillus st Q99up4 staphylococ P45390 escherichia P21159 myxococcus P12342 bos taurus
TRFL_BUBBU VIA_BBNV PIPĀ DROME PHYC_ORYSA BP28_DROME RL28_BACST RL28_LISMO RL28_LISMO RL28_STAMO YRBC_ECOLI PDXH_MYXXA II22A_BOVIN
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ALIGNMENTS

RESULT 1

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_	15-JUL-1999 (Rel. 38,
	late)
	GN LIF OR LF.
_	Homo sapiens (Human)
	Eukaryota; Metazoa; Chordata;
_	Mammalia; Eutheria; Primates;
	NCBI_TaxID=9606;
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	Doy M W Wolchill G T 3- 2- 2- 2-
	"Complete nucleotide semional of bush a pieper F.R.;
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	kL Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
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PK	RP SEQUENCE FROM N.A.
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ρζ	RT "Human neutrophil lactoferrin coding and 5' flanking region DNA
 p< t	sequences.";
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KA F	Cheng H., Chen X., Huan L.;
. I.G.	Submitted (DEC 2000)
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Page

SEQUENCE OF 3-711 FROM N.A.

TISSUE=Mammary

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McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Mian M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzzy D., Chen C.N., Brans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Diagarpan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The present state of the human lactotransferrin sequence. Study alignment of the cyanogen bromide fragments and characterization N- and C-terminal domains.";
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MEDLINE=91156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rado T.A., Wei X., Benz E.J. Jr., "Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
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253-->methionine mutant.";
                                                                                                                                                                                                                       SEQUENCE OF 20-711.

MEDLINE=85076667; PubMed=6510420;
Metz-Boutique M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530.
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"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jolles P.,
"An 88 amino acid long C-terminal sequence of human
                                                                                              Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochim. Biophys. Acta 670:243-254 (1981)
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MEDLINE=99190892; Pubmed=10089347;
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                                                                                                                                                                       Nucleic Acids Res. 18:4013-4013(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Biochem. 145:659-666(1984),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=82046817; PubMed=6794640;
                                      TISSUE=Mammary gland;
MEDLINE=90326549; Pubmed=2374734;
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AF332168; AAG48753.1; BC015822; AAH15822.1; BC015823; AAH15823.1; --

EMBL; EMBL; EMBL; EMBL;

M73700; AAAS9479.1; -. X52941; CAA37116.1; -. U95626; AAB57795.1; -.

EMBL; EMBL; 31-AUG-94. 31-OCT-93.

S11228; LLCF; 1LFG; 1LFH; 1LFI; 1LGB; 1LGC; 1BKA; 1DSN;

PIR; PDB; PDB; PDB;

31-0CT-93. 31-0CT-93. 31-AUG-94

PDB; PDB; PDB; PDB; PDB; PDB; PDB;

EMBL; U07643; AAB60324.1; BMBL; M93100; AAA36159.1; BMBL; M3202; AAA5855.11; BMBL; M3205; AAA58656.1; BMBL; M18642; AAA86665.1; ---

EMBL; X53961; CAA37914.1; -.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: TRANSFERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH
-2N BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-1- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST
ACTIVITY: LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE
LACTOFERROXIN B AND C HAVE SOMEWHATH HIGHER DEGREES OF PREFERENCE
FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                         CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Jun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                        Cunsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y., Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F., El Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K., "Heitmancik J.F., Teng C.T., Teng C.T., "Familial subepithelial corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene."; Mol. Vision 4:31-32(1998).
                                                                                                           MEDLINE-99192677; PubMed-10089508; Jameson G.B., Andersen B.F., Norris G.E., Thomas D.H., Baker E.N.; Jameson G.B., Anderseon B.F., Norris G.E., Thomas D.H., Baker E.N.; "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                            X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                from human lactoferrin,";
Agric. Biol. Chem. 54:1803-1810(1990).
                                                          Acta Crystallogr. D 55:403-407(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                          Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Somall; TISSUE=Lactating mammary gland; Kappeler S.R., Ackermann M., Farah Z., Puhan Z.; "Sequence analysis of camel (Camelus dromedarius) lactoferrin."; Int. Dairy J. 9:481-486(1999).
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Pfam; PF00145; transferrin, 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
TRANSFERRIN. 3; 2.
TRANSFERRIN. 3; 2.
                                           0;
   Query Match 95.8%; Score 68; DB 1; Length 711; Best Local Similarity 91.7%; Pred. No. 0.00024; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN
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EMBL; AF165879; AAF82241.1; -.
HSSP; O77811; 1B1X.
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TISSUE-Mammary gland;
MEDLINE-94380047; PubMed=8093048;
le Provost F., Nocart M., Guerin G., Martin P.;
Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 synteny group.";
Biochem. Biophys. Res. Commun. 203:13241332(1994).
I- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORT PROTEINS WHICH CAN BIND TWO ALONS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARRONATE.
SUBUNIT: MONOWER (BY SIMILARITY).
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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G -> A (IN REF. 2).

G -> B (IN REF. 2).

ILLS -> PLF (IN REF. 2).

L -> F (IN REF. 2).

A -> P (IN REF. 2).

A -> Q (IN REF. 2).

A -> Q (IN REF. 2).

A -> Q (IN REF. 2).

W; 0BOCL75A0B69D430 CRC64;
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                          IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 2 (BY SIMILARITY)
ANION (BY SIMILARITY)
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ID TRFL_CAPHI

AC Q29477; Q29479;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-UNN-2002 (Rel. 41, Last annotation update)

DI 15-JUN-2002 (Rel. 41, Last annotation update)

DI actotransferrin precursor (Lactoferrin).
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us-09-743-107b-81.rsp

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RESULT 4
TRFL MOUSE
                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
                                                                                                              EMBL, X78902; CAASSSI7.1; -.
EMBL, X78902; CAASSSI7.1; -.
Interpror, IPRO91156; Transferrin.
Ffam, PRO0405; transferrin; 2.
PRINTS; PRO0422; TRANSFERRIN.
SNART; SN00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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L -> R (IN REF. 2).
Q -> K (IN REF. 2).
S -> P (IN REF. 2).
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D -> G (IN REF. 2).
I, FZEDA3CB3539960D CRC64;
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 DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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63.6%;
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MEDIJINE=92042099; PubMed=1939212;

Liu Y., Teng C.T.;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266.21880-21885(1991)

-i- FUNCTION: TRANSPERSING ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                            Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Pentecost B.T., Teng C.T., "Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
               MORDATE, PORGOO, GG1799; Q922P2; C1-AVG-1988 (Rel. 08, Created) 15-UNA-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN.
707 AA.
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MD) MG1:9687; Ltf.
InterPro; IPR001156; Transferrin.
Ffam; PF00405; transferrin, 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
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EMBL, D88510; BAA13633.1; -.
EMBL, BC006904; AAH66904.1; --
EMBL, M7478; AAA39427.1; --
PIR; A28438; A28438.
STANDARD;
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TRFL MOUSE
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SIGNAL
CHAIN
REPEAT
                     HILLER BERNER BE
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Gaps

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1; Indels

Mismatches

3,

Conservative

Matches

1 CFOWOKONMRKV 11 CYOWORRMRKL 48

à g

38

us-09-743-107b-81.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORE TOWARDS THE MINUS ENDS OF MICROTUBULES. DYNEIN HAS AFPASE ACTIVITY.
SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
                                                                                                                                                                                                                                                                                                            (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 45; DB 1; Length 707;
Pred. No. 2.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                            77865 MW; F26AE0340A4C19A8 CRC64;
                                                                                                                                                                                                                                                                                  ANION (POTENTIAL).

N-LINEED (GLCNAC. .) (1

N-LINKED (GLCNAC. .) (1

MR -> IQG (IN REF. 1).

R -> Q (IN REF. 2).

M -> L (IN REF. 2).

M -> L (IN REF. 2).

A -> D (IN REF. 2).

B -> G (IN REF. 1).

C -> D (IN REF. 2).

C -> D (IN REF. 2).

C -> D (IN REF. 1).

C -> D (IN REF. 1).

C -> D (IN REF. 1).
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2 (BY SIMILARITY).
2 (BY SIMILARITY).
3 (BY SIMILARITY).
5 (BY SIMILARITY).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
   2.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 4568 AA
                                                                                                                                                                               BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
                                                                                                                                                                                           IRON 1
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IRON 2
IRON 2
IRON 2
IRON 2
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MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                                                                                                                                                                                63.4%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                              359
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629
707 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQKNWRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37 CLRWQNEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain genes.";
J. Cell Sci. 1
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Q39565;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             resolution.";
J. Mol. Biol. 289:303-317(1999).

-1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-CAN BIND TWO ANONS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=99296631; PubMed=10366507;
Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eŭkaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus
                                                                                                                                                                                                                                          COILED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
MICROTUBLIA-BINDING (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COILED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
COLLED COIL (POTENTIAL).
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .,
                                                                                                                                                EMBL; U02963; AAA19956.1; -.
InterPro; IPR004273; Dynein_heavy.
Pfam; PP03028; Dynein_heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Colled coil.
DOMAIN 277 293 COILED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.4%; Score 45; DB 1; Length 4568; 50.0%; Pred. No. 15;
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                 ATP (POTENTIAL)
ATP (POTENTIAL)
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                                                                                                                                                                                                                               COILED COIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                               519961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 50.0
les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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1825
2045
2848
3162
3425
3728
1926
2209
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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3106
3339
3648
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TRFL_HORSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                    PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 2; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.

Signal; 3D-structure.

SIGNAL < 1 1 1
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.6%; Score 43; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07BB84D50E1B165D CRC64;
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(GLCNAC. . .)
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(BY SIMILARITY)
                                                                                                                                                                                                                      LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 5.1;
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N-LINKED
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                                                                                                                 InterPro; IPR001156; Transferrin. Prem; Pr00405; transferrin; 2. PRINTS; PR00422; TRANSFERRIN. SMART; SM00094; TR FER; 2.
                                                                              EMBL; AJ010930; CAA09407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHYC_SORBI STANDARD;
P93558;
16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3.,
1. Conservative
                                                                                                                                                                                                                                                                PDB; 1B1X; 02-DEC-98.
PDB; 1B7U; 02-FEB-99.
PDB; 1B7Z; 02-FEB-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CFQWQKNMRKVR 12
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                                                                        Sorghum bicolor (Sorghum) (Sorghum vulgare).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACC clade,
                                                                                                                                                                                                                                                                                           PUTCHING B.",
PLATE PHYSIOL 113:611-619(1997).

-I FUNCTION: REGULARDRY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTROM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR INDUCTS AN ARRIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR INDUCTS AN ARRAY OF MORPHOGENIC RESPONSES, WHEREAS RECONVERSION OF PRR TO PR CANCELS THE INDUCTION OF THOSE RESPONSES, PER CONTROLS THE EXPRESSION OF A NUMBER OF NUCLEAR GENES INCLUDING THOSE ENCODING THE SMALL SUBDMIT OF RIBLICOSE—BISPHOSPHATE CARBOXYLASE, CHLOROPHYLLI A/B BINDING PROTEIN, PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS THE EXPRESSION OF ITS OWN GENE (S) IN A NEGATIVE FEEDBACK FASHION (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER (BY SIMILARITY).
PTM: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.
SIMILARITY: BELONGS TO THE PHYTOCHROME FAMILY.
SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
                                                                                                                                                                                                                MEDLINE=97198556; PubMed=9046599;
Childs K.L., Miller F.R., Cordonnier-Pratt M.-M., Pratt L.H.,
Morgan P.W., Mullet J.E.;
"The Sorghum bicolor photoperiod sensitivity gene, Ma3, encodes a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PEAM; PRO1599; GAF; 1.

PEAM; PRO1518; HATPABSE_c; 1.

PRINTS; PRO1033; PHYTOCHROME.

SMART; SM00065; GAF; 1.

SMART; SM00088; HisRA; 1.

SMART; SM00086; PAC; 1.

SMART; SM00091; PAS; 2.

TIGREAMS; TIGR00229; SENSOTY_box; 2.

PROSITE; PS50112; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, US6731; AAB41399.1; ...
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003018; GAF.
InterPro; IPR004359; HIS KIN sig.
InterPro; IPR003661; His Kin sig.
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR001294; PAS domain.
Pfam, PF00360; phytochrome.
Pfam, PF00360; phytochrome; 1.
Pfam; PF00369; phytochrome; 1.
                                                                                                                                       Panicoideae; Andropogoneae; Sorghum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Repeat; Multigene family.
DOMAIN 618 688
16-OCT-2001 (Rel. 40,
15-JUN-2002 (Rel. 41,
Phytochrome C.
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                            NCBI_TaxID=4558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
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HISTIDINE KINASE

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Pfam; PF03550; LolB; 1.
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                                                                                                                                                                                        cholerae.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21992816; PubMed=11997336; Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Mang J., Yu J., Yang H.; "A complete sequence of T. tengcongensis genome."; Genome Res. 12:689-700(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
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0
                                                                 Score 39; DB 1; Length 1135;
Pred. No. 41;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
  321 321 CHROMOPHORE (BY SIMILARITY).
1135 AA; 126315 MW; AFCC934B7592DE4D CRC64;
                                                                                                                3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        53.5%; Score 38; DB 1; Length 62; 60.0%; Pred. No. 3.3; Live 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
So ribosomal protein L28.
RPMS OR TTEL495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOLB VIBCH STANDARD; PRT; 211 AA. 16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Outer-membrane lipoprotein lolb precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, AE013107, AAM24713.1; -. Ribosomal protein; Complete proteome. SPOITENCE 62 AA; 7037 MW; CAADB6050
                                                                                                                                                                                                                                                                                                  PRT;
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STRAIN=El Tor N16961 / Serotype Ol;
MEDLINE=20406833; PubMed=10952301;
                                                               54.9%;
                                                                                                       5; Conservative
                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                    775 CLEWNKAMOKI 785
                                                                                                                                            1 CFOWOKNYRKV 11
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=119072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                     SEQUENCE
BINDING
                                                                                                                                                                                                                                                                                                             QBR9U1;
                                                                                                  Matches
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Heidelberg J.F., Bisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Einolaeva R.R., Nelson K.E., Read T.D., Tettelin H., Richardson D. Emolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salbberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
Nhite O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.,
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chaperone; Outer membrane; Lipoprotein; Transport; Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                      Nature 406:477-483(2000)

-!- FUNCTION: PLAYS A CRITICAL ROLE IN THE INCORPORATION OF

LIPOPROTEINS IN THE OUTER MEMBRANE AFTER THBY ARE RELEASED BY

THE LOLA PROTEIN (BY SIMILARITY)

-!- SUBCELLULAR LOCATION: Attached to the outer membrane by a lipid
                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 26 BY SIMILARITY.
27 211 OUTER-MEMBRANE LIPOPROTEIN LOLB.
27 27 N-ACYL DIGLYCERIDE (BY SIMILARITY).
211 AA; 24379 MW; FIEF70858484177E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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16-OCT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
-!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP +
diphosphate + L-histidy1-tRNA(His).
-!- SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.5%; Score 38; DB 1; Length 211; 60.0%; Pred. No. 11;
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anchor (By similarity).
-!- SIMILARITY: BELONGS TO THE LOLB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   428 AA
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                                                                                                                                                                                                                                                                              Oxidoreductase; NAD; Ubiquinone; Transport; Sodium transport;
Flavoprotein; FMN; Transmembrane; Inner membrane; Complete proteome.
TRANSMEM 13 35 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP).
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Portnoy D.A., Erickson A.H., Kochan J., Ravetch J.V., Unkeless J.C.,

"Cloning and characterization of a mouse cysteine proteinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Comparison of cathepsin L synthesized by normal and transformed
cells at the gene, message, protein, and oligosaccharide levels.";
Arch. Biochem. Biophys. 283:447-457(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Denhardt D.T., Hamilton R.T., Parfett C.L.J., Edwards D.R., Pierre R.S., Waterhouse P., Nilson-Hamilton M.; "Close relationship of the major excreted protein of transformed murine fibroblasts to thiol-dependent cathepsins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-88076849; PubMed=3689328;
Troon B.R., Gal S., Gottesman M.M.;
"Sequence and expression of the cDNA for MEP (major excreted protein), a transformation-regulated secreted cathepsin.";
Biochem. J. 246:731-735 (1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joseph L.J., Chang L.C., Stamenkovich D., Sukhatme V.P., "Complete nucleotide and deduced amino acid sequences of hum murine preprocathepsin L. An abundant transcript induced by transformation of fibroblasts.", Clin. Invest. 81:1621-1629(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 316;
                                                                                                                                                                                                                                                                                                                                           35 POTENTIAL.
280 FMN (BY SIMILARITY).
34412 MW, 4AA9442245DE6250 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A., AND CARBOHYDRATE-LINKAGE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-1988 (Rel. 06, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37; DB Pred. No. 25;
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MEDLINE=88213715; PubMed=2835398;
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                                                                                                                                                                                                                                                   EMBL; AE001300; AAC67872.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52.1%;
85.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
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280
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                                                                                                                                                                                                                                                                                                                                                                                                           316 AA;
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P06797;
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                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR002106; AAKENNA ligaseII.
InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004154; HGTP anticodon.
InterPro; IPR002314; HRNS-
InterPro; IPR002314; HRNS-synt 2b.
Pfam; PF00587; RRNA-synt 2b; 1.
Pfam; PF00159; HGTP anticodon; 1.
IIGRAMs; TIGR00442; hiss;
PROSITE; PS50862; AA TRNA, LIGASE II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, last annotation update)
Probable Na(+)-translocating NADH-quinone reductase subunit C
(EC 1.6.5.-) (Na(+)-translocating NQR subunit C) (Na(+)-NQR subunit C)
(NQR complex subunit C) (NQR-1 subunit C).
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-1- SUBCELLULAR LOCATION: Cytoplasmic.
-1- SIMILARITY: BELONGS TO CLASS-11 AMINOACYL-TRNA SYNTHETASE FAMILY.
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Science 282:754-759(1998).
-1- FUNCTION: NOR COMPLEX CATALYZES THE REDUCTION OF UBIQUINONB-1 TO UBIQUINOL BY TWO SUCCESSIVE REACTIONS, COUPLED WITH THE TRANSPORT OF NA(+) IONS FROM THE CYTOPLASM TO THE PERIPLAM. NORA TO NORE ARE PROBABLY INVOLVED IN THE SECOND STEP, THE CONVERSION OF UBISEMIQUINONE TO UBIQUINOL (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- COFACTOR: FWN (BY SIMILARITY).
-!- SUBUNIT: COMPOSED OF SIX SUBUNITS; NQRA, NQRB, NQRC, NQRD, NQRE
AND NQRF (BY SIMILARITY).
-!- SUBCELLUIAR LOCATION: Inner membrane (Potential).
-!- SIMILARITY: BELONGS TO THE NQRC FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: NADH + ubiquinone + Na(+) (In) = NAD(+) + ubiquinol + Na(+) (Out).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38; DB 1; Length 428;
Pred. No. 23;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9CFS59ED0E689DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chlamydia trachomatis.
Bacteria, Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        316 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 40, Last sequence update) (Rel. 40, Last annotation update
                                                                                                                                                                                                                                                                                            or send an email to license@igb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                            EMBL; AE002349; AAF39630.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48939 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
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55.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 032422; 1QE0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            428 AA;
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SEQUENCE 428 AA
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                                                                         -!- CATALYTIC ACTIVITY: Specificity close to that of papain. As compared to cathepsin B, cathepsin L exhibits higher activity towards protein substrates, but has little activity on Z-Arg-Arg-NHMec, and no peptidyl-dipeptidase activity.
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Cancer Res. 46:4590-4593(1986).
-!- FUNCTION: IMPORTANT FOR THE OVERALL DEGRADATION OF PROTEINS IN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
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                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: LYBOSOMA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X06086; CAA29470.1; -.
EMBL; J02583; AAA37445.1; -.
EMBL; M20495; AAA39984.1; -.
EMBL; X04392; CAA27980.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37547 MW;
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PIR; S13890; S13890.
HSSP; P07711; 1CJL.
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MEROPS; C01.032;
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CONFLICT
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CATL RAT STANDARD; PRT; 334 AA.
P07154; Q9QV07;
01-APR-1988 (Rel. 07, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP)

|:|||| :: 52 WEKNMRMIQ 60

RESULT 13 CATL_RAT Rattus norvegicus (Rat).

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Zabludoff S.D., Charron M., Decerbo J.N., Simukova N., Wright W.W.; "Male germ cells regulate transcription of the cathepsin L gene by rat Sertoli cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kawada A., Hara K., Kominami B., Tezuka T., Takahashi M., Takahara H.,
"Precursor of rat epidermal cathepsin L: purification and
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L is lysosomal.

-I- TISSUE SPECIFICITY: Both mature cathepsin L and procathepsin L are found in the upper epidermis. The lower epidermis predominantly contains procathepsin L. In seminiferous tubules expression is greater at stages VI-VII than at stages IX-XII.

-I- INDUCTION: Expression in Sertoli cells is repressed by germ cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Procathepsin L is secreted. Mature cathepsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papadopoulos \bar{\mathbf{v}}., "Identification of a stimulator of steroid hormone synthesis isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of steroidogenesis by TIMPI.
-!- CATALYTIC ACTIVITY: Specificity close to that of papain. As compared to cathepsin B, cathepsin L exhibits higher activity towards protein substrates, but has little activity on Z-Arg-Arg-NHMec, and no peptidyl-dipeptidase activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92168015, PubMed=1791830;
Erickson-lawrence M., Zabludoff S.D., Wright W.W.;
Cyclic protein-2, a secretory product of rat Sertoli cells, is the
proanzyme form of cathepsin L.";
Mol. Endocrinol. 5:1789-1798(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Towatari T., Katunuma N.;
"Amino acid sequence of rat liver cathepsin L.";
FEBS Lett. 236:57-61(1998).
-!- FUNCTION: Important for the overall degradation of proteins in lysosomes. Procathepsin L is required for maximal stimulation
                                                                                                                                                 Katunuma N ,, Suzuki K.;
"Molecular cloning and sequencing of cDNA for rat cathepsin L.";
FEBS Lett. 223:69-73(1987)
                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINES-90092543; PubWed=2599113;
Ishidoh K., Kominami B., Suzuki K., Katunuma N.;
"Gene structure and 5-upstream sequence of rat cathepsin L.";
FEBS Lett. 259:71-74(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 18-37, FUNCTION, AND SUBCELLULAR LOCATION.
STRAIN=Sprague-Dawley, TISSUE=Sertoli cells,
MEDLINE=92296691, PubMed=7777858;
Boujrad N., Ogwuegbu S.O., Garnier M., Lee C.-H., Martin B.M.,
                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-42 FROM N.A., TISSUE SPECIFICITY, AND INDUCTION
                                                                                                                               Ishidoh K., Towatari T., Imajoh S., Kawasaki H., Kominami
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 18-28, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley, TISSUE=Epidermis;
MEDLINE=20164186; PubMed=10699763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  localization.";
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21255611; PubMed=11356678;
                                                                                            STRAIN=Wistar; TISSUE=Kidney;
MEDLINE=88030047; PubMed=3666143;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Endocrinology 142:2318-2327(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Liver;
MEDLINE=88296890; PubMed=3402618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dermatol. Sci. 23:36-45(2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 88-334 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 268:1609-1612(1995).
                                                                                                                                                                                                                                                                                                                                                        STRAIN=Sprague-Dawley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Sertoli cells;
                       Mammalia, Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunohistochemical
                                                                         SEQUENCE FROM N.A.
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Query Match
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                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                            PRINTS; PR00705; PAPAIN.
PRODOM; PD000158; Peptidase C1; 1.
PROSITE; PS00139; THIOL_PROTEASE C7S; 1.
PROSITE; PS00649; THIOL_PROTEASE_ASN; 1.
PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.
Hydrolase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
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CATHEPSIN L, LIGHT CHAIN.
BY SIMILARITY.
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A SIMILARITY.
N-LINKED (GLONG.).
A -> P (IN REF. 1).
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Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases -!- SIMILARITY: BELONGS TO THE OKL38 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37660 MW; AFFA997582E34AF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                ACTIVATION PEPTIDE
  -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein F30B5.4 in chromosome IV
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                                                                                                                                                                                                                      InterPro; IPR000668; Peptidase C1.
InterPro; IPR000169; SHprot acsite.
Pfam; PF00112; Peptidase C1; 1.
                                                                                                                                                     EMBL; AF025476; AAB81616.1; -.
EMBL; S85184; AAB21516.1; -.
PIR; S07098; KHRTL.
                                                                                                                                        EMBL; Y00697; CAA68691.1; -.
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                                                                                                                                                                                               HSSP; 060911; 1FH0.
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                                                                                                                                                                                                           MEROPS; C01.032;
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219910;
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ACT_SITE
ACT_SITE
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RA MEDDINE=21846401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ragouroe U., Peat N., Rajandream M.A., Lyne M., Lyne R., Stewart A., Ragouroe U., Peat N., Radyles U., Basham D., Bowaman S., Raderles R., Brown D., Brown S., Chillingworth T., Churcher C.M., Raderles R., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Raderles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Raderles E., Moules L., Jones M., Leather S., McDonald S., McLean J., Radorey P., Moule S., Mungall K., Murphy L., Niblett D., Odell C., Raderson D., Quail M.A., Rabbinowitsch E., Raderson D., Quail M.A., Rabbinowitsch E., Saunders D., Seeger R., Staren S., Stevens K., Starp S., Stevens K., Starp S., Stevens K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S., McGodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Radel J., Volckaert G., Aert R., Robben J., Grymonprez B., Rodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Radel J., Langer I., Beck A., Lehrach H., Reinhardt R., Purnelle B., Rader P., Zimmermann W., Wedder H., Wambutt R., Purnelle B., R. Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S., Lous M., Rochet M., Galtor M., Galzon A., Cadieu E., Jimenez J., Sanchez M., del Rey F., Benito J., Rorutti I., Lowe T., Moreno S., Armstrong J., Porsburg S.L., R. Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., The Genome sequence of Schizosaccharomyces pombe.";
R. Matter 415:811-880(2002).
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the Swiss Institute of Bioinformatics and the EMBL outstation
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-!- SIMILARITY: BELONGS TO THE ERA/TRME FAMILY OF GTP-BINDING
                                                                                                                                                                                                                                                                                                     DB 1; Length 455;
                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                            WormPep, F30B5.4, CE28552.
Hypothetical protein.
SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes, Schizosaccharomycetales, Schizosaccharomycetaceae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTPase MSS1 homolog, mitochondrial precursor
                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                  Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                     52.1%;
50.0%;
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                                                                                                                                                                          EMBL; U42437; AAA83493.2; -.
                                                                                                                                                                                                                                                                                                                                                    5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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Best Local Similarity 41.7%; Pred. No. 40;
Matches 5; Conservative 4; Mismatches 3; Indels
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Search completed: February 21, 2003, 07:27:57 Job time : 6.6 secs

||:|:| 178 CFRWRKKLIEYR 189 1 CFOWOKNIMRKVR 12

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Sequence:

Title:

Run on:

Searched:

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QBUIC2 agrobacteri
Q92rhB rhizobium m
Q89fk3 brucella me
Q96f19 mycoplasma
Q96f02 arabidopsis
Q92k94 helicobacte
Q97rg8 clostridium
Q97rg8 clostridium
Q97rg8 olostridium
Q97rg8 olostridium
Q97rg9 homo sapien
Q9797 homo sapien
Q9295 chlamydia p
Q9f19 arabidopsis
Q19153 caenorhabdi
Q23230 arabidopsis
Q90863 human immun
Q90884 human immun
Q90886 inckettsia
Q8c55 strz conver
Q97177 sulfolobus
Q72904 human immun
                            Q9sz87 arabidopsis
Q8r9ul thermoanaer
Q9xhpl sesamum ind
Q9apz3 vibrio chol
Q986a0 rhizobium l
  Q8yp77 anabaena sp
Q8rgt4 fusobacteri
Q8s013 oryza sativ
                                                                                                                                                                                                                                                          28rmb8 cytophaga j
                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEOURNCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                    QBTCD2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UNN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
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                                                      Q9APZ3
Q986A0
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092955
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Q8R9U1
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Q92RH8
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Q9C6N2
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097TQ8
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090884
Q92GL6
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Q971N7
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Q9NZW3
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16
                                   PRELIMINARY;
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Best Local Similarity
Lactotransferrin.
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Q9UCY5;
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O9tr80 ovis aries
O8xse2 ralstonia s
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Q9hpa3 halobacteri
Q93780 caenorhabdi
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Q9q910 human immun
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Q9nus2 homo sapien
Q96m21 homo sapien
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Q9xvd1 caenorhabdi
                                                    February 21, 2003, 07:25:55; Search time 20.8 Seconds (without alignments) 118.873 Million cell updates/sec
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 GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                     Total number of hits satisfying chosen parameters:
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Q9UCY5
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Q8Z462
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Q9LTN4
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Q9WYQ1
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Aslanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S., Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L., Chadler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N., Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T., Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;

"Genome sequence of the plant pathogen Ralstonia solanacearum.";

"Astale J. 1977-502 (2002)

"BME, AL646079; CAD17685.1; -..

"InterPro; IPR004844; S/T_phosphtse.

"InterPro; IPR004844; S/T_phosphtse.

"InterPro; IPR004844; S/T_phosphtse.

"Plani, PF00149; Metallophos; 1.

"Planid; Complete protecome.

"Weight Supplier Protecome."
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50.0%; Pred. No. 6.6;
ive 2; Mismatches 4;
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01-NOV-1999 (TrEMBLrel. 12, Li
01-MAR-2002 (TrEMBLrel. 20, Li
C24H11.8 protein.
Caenorhabditis elegans.
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
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Q38115;
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                                                                                                                                                Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
Bovidae; Caprinae; Ovis.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                              83.1%; Score 59; DB 4; Length 38; 90.9%; Pred. No. 0.001;
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Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP; 077698; 1CE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MXY-2000 (TrEWBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UDN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ICC protein homolog.
ICC OR RSP0534 OR RS00414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ralstonia solanacearum (Pseudomonas solanacearum).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                                                                 seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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MEDLINE=21681879; PubMed=11823852;
                                                                                                                    MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; 077698; ICE2.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 90.9
nes 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 72.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FOWOKNIMIKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 FÓWÓRNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWQKNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 CYQWOKKMRKL 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid megaplasmid
                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ovis aries (Sheep)
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                              NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                     Pfam;
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Matches
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9997R90

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                                                                                                                                                                                                                                                                                                                                                   MEDLINE=96332668; PubMed=8730874;
Nauta A., Van Sinderen D., Karsens H., Smit B., Venema G., Kok J.;
Nauta A., Van Sinderen D., Karsens H., Smit B., Venema G., Kok J.;
Inducible gene expression mediated by a repressor-operator system isolated from Lactococcus lactis bacteriophage rlt.";
Mol. Microbiol. 19:1331-1341(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJURE-96332669; PubMed-8730875; Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H., Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H., Venema G., Nauta A.; Requence analysis and molecular characterization of the temperate lactococcal bacteriophage r1t."; Mol. Microbiol. 19:1343-1355 (1996).
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60.0%; Pred. No. 11;
iive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U38906; AAB18704.1; -.
SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;
                                                                                               Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
   469 AA.
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AN SUBLINE-20504483; PubMed=11016950; RA MEDLINE-20504483; PubMed=11016950; RA MEDLINE-20504483; PubMed=11016950; RA MEDLINE-20504483; PubMed=11016950; RA MG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pabrona J., RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J., RA Leithauser B., Keller K., Cruz K., Danson M.G., Hough D.W., RA Leithauser B., Kaller K., Cruz K., Danson M.G., Hough D.W., RA Benbarger T.A., Peck R.F., Pohlschroder M., Spudioh J.L., Jung K.-H., RA Lembarger T., Hou S., Danlels C.J., Dennis P.P., Cmer A.D., RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; "Genome sequence of Halobacterium species NRC-1."; "Matl. Acad. Sci.U.S.A. 97:12176-12181(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.2%; Score 42; DB 17; Length 584; 50.0%; Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dobson k.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                              Halobacterium sp. (strain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               584 AA; 65151 MW; 21BF5D5F0486CCC6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81089; CAB03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
              (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1997 (TrEMBLrel. 02, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 1711. BMBL, AE005048, AAG19967.1, -
InterPro. IPR001646; Speptide repeat.
InterPro. IPR001622; K+channel pore.
Pfam, PF00805; Pentapeptide; 2.
Complete proteome.
EQUENCE 584 AA, 65151 MW, 21BF5D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                       Halobacteriaceae; Halobacterium.
NCBI TaxID=64091;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 63.6 tes 7; Conservative
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Best Local Similarity
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                01-MAR-2001
01-MAR-2001
                                                        01-MAR-2002
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Matches
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STRAIN=CT18;

MEDLINE=21534947; PubMed=11677608;

MEDLINE=21534947; PubMed=11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Crohin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Whitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Bacteria, Proteobacteria, gamma subdivision, Enterobacteriaceae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                               "Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                              Similarity 70.0%; Pred. No. 17; Conservative 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59.2%; Score 42; DB 16; Length 511; 58.3%; Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Indels
                                                                             Lloyd C.R.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                 Pfam; PF00520; ion trans; 1. - SEQUENCE 681 AA; 78178 MW; D36AC05C3FA029CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nature 413:848-852(2001).

EMBL, AL627276; CAD06049.1; -.

Hypothetical protein; Complete proteome.

SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            511 AA
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0; Mismatches
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81475; CAB03914.1;
InterPro; IPR001622; K+channel pore.
InterPro; IPR000636; M+channel nlg.
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                                                                                                                                                          MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
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                                                                                                                                     SEQUENCE FROM N.A.
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                                                        SEQUENCE FROM N.A.
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                      CBI_TaxID=6239;
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Matches
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RESULT 7

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Q8Z462

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262 FQWKISMRKTR 272

2 FOWOKONMRKVR 12

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584 AA.

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PRELIMINARY;

09HPA3 ID 09HPA3 AC 09HPA3;

RESULT 8

Best Loca Matches

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"Structural analysis of Arabidopsis thaliana chromosome 5, X. Sequence features of the regions of 3,076,755 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                            STRAIN=COLUMBIA;
BEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ11175 fis, clone PLACE1007375, weakly similar to phorbol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.3%; Score 40; DB 10; Length 121; 60.0%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56.3%; Score 40; DB 4; Length 306; 55.6%; Pred. No. 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025708; AAH25708.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lecurations.";
clones.";
DNA Res. 7:31-63(2000).
EMBL; AB024037; BAA97406.1; -.
EMBL; AB024037; BAA97406.1; -.
"Anteng 121 AA; 13798 MW; 3DEE6D4A539D2933 CRC64;
"Anteng 121 AA; 13798 MW; 3DEE6D4A539D2933 CRC64;
"Anteng 121 AA; 13798 MW; 3DEE6D4A539D2933 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QBTAX2;.
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ11175.
                                                    121 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2; Mismatches
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFOWOKUMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=PANCREAS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  269 CFOWESTLR 277
                                                                                                                                                                                                                                                                                        NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWOKNMR 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                               Q9LTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8TAX2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9NUS2
RESULT 12
Q9LTN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
Q9NUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                             Zea mays (Maize).
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoli.ophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tanuri A., Machado E., Caride B., Costa L.J., Telles J.G.;
"Primary infections with HIV-1 of women and their offspring in Rio de Janeiro, Brazil: Finding of recombinant of HIV-1 subtypes B and F.";
Submitted (MAY-1999) to the BMBL/GenBank/DDBJ databases.
InterPro; IPR000777; GP120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.3%; Score 40; DB 15; Length 115; 60.0%; Pred. No. 9.1;
                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. B73;
Ramakrishna W., SanMiguel P., Emberton J., Bennetzen J.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=CV. B73;
Llaca V., Linton E., Young S., Kovchok S., Messing J.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF466202, AAL75475.1; -.
SEQUENCE 570 AA, 63178 MW; AIBEF8390F0BA3F5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 AA; 12832 MW; 86E509D6F6978127 CRC64;
                                                                                                         01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
puttive aldose reductase-related protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAX-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                 570 AA
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AIDS; Coat protein; Glycoprotein.
                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                    01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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61 QWEKTLROVR 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11676;
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SEQUENCE
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       RESULT 10
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AC 08548
AC 08548
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DT 01-JUD
DT 01-JUD
DE DLACT
CC BUKART
CC STRAIT
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RESULT 11

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Gaps

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Gaps

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ester/diacylglycerol-binding protein UNC-13

us-09-743-107b-81.rspt

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66 CFQWRWGVRYLR 77
1 CFQWQKNWRKVR 12
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6; Conservative

Matches

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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

ENBL; AK057453; BAB71493.1; --

SEQUENCE 274 AA; 30083 MW; IDP43654D4135B2F CRC64;
                                                                                                                            TISSUB=PLACENTA,

IBOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,

Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Yamamoto J., Wakamatu A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.,

Ninomiya K., Iwayanagi T.,

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                     Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OS6M21;

01-DEC-2001 (TrEMBLrel. 19, Created)

01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

CDNA FLJ32891 fis, clone TESTI2004929.

Homo mapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HSSP; P21707; 1BYN.
InterPro; IPR000008; C2.
InterPro; IPR000604; C2.
Effan; PR00168; C2; 1.
PRINTS; PR00168; C2; 1.
PRINTS; PR00160; C2DOMAIN.
SMRRT; SM00299; C2; 1.
PROSITE; PS00499; C2 DOMAIN 1; UNKNOWN 1.
PROSITE; PS000030; RRM_RNP 1; UNKNOWN 1.
SRQUENCE 466 AA; 53192 MW; E4113A5062F5BD6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.3%; Score 40; DB 4; Length 466; 55.6%; Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Indels
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Best Local Similarity
Matches 5; Conserv
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                                                                                                              SEQUENCE FROM N.A.
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                                                                           NCBI_TaxID=9606;
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Search completed: February 21, 2003, 07:44:36 Job time : 21.8 secs
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Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
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Synthetic.
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17-JUL-1998;
29-DEC-1998;
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Human lactoferrin
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                                                                                               February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
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1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1981.DAT:*
3: /SIDS2/gcgdata/geneseqg/emseqp-embl/AA1981.DAT:*
4: /SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*
5: /SIDS2/gcgdata/geneseqg-embl/AA1981.DAT:*
5: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1981.DAT:*
7: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1986.DAT:*
8: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1980.DAT:*
9: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1980.DAT:*
10: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1980.DAT:*
11: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1980.DAT:*
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13: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1993.DAT:*
14: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1992.DAT:*
15: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1992.DAT:*
16: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1992.DAT:*
17: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1996.DAT:*
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18: /SIDS2/gcgdata/geneseqg/geneseqp-embl/AA1996.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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AAY78049
AAY78036
AAY78050
AAY78051
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Peptide for anti-u Human lactoferrin Human lactoferrin	Human lactoferrin Human lactoferrin Human lactoferrin			Human lactoferrin Human lactoferrin	υ	Human lactoferrin	Himan lactoferrin	Ε	Lactoferrin-relate	Lactoferrin derive				lacto	Bovine lactoferrin	ത	Anti-parasitic lac	Peptide for anti-u	Lactoferrin-derive	Lactoferrin-derive	Lactoferrin derive	- 1	Lactoferrin-derive	Lactoferrin deriva		Thrombus formation	Lactoferrin hydrol
AAR9855 AAY7803 AAY7806	1 AAY78063 1 AAY78031 1 AAY78064		AAY7806	AAY/806/ 5 AAR69352	·	1 AAY78033		3 AAR21810			5 AAR48531						AAR8026	-	AAR9185	•			AAR87622	AAW26150	AAW14036	-	
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ALIGNMENTS

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative Human lactoferrin derived peptide SEQ ID NO:82. AAY78082 standard; Peptide; 12 AA. 98SE-0002441. 98SE-0002562. 98SE-0004614. 99WO-SE01230.

WPI; 2000-147388/13.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the dirculation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula sloo be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin will offer an order of the control of the same purposes as lactoferrin at lower
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             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 70; DB 21; Length 12; 100.0%; Pred. No. 1.7e-05; ative 0; Mismatches 0; Indels
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                                                                   Claim 22; Page 36; 102pp; English.
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98SE-0004614.
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human

Claim 12; Page 70; 102pp; English

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Bven though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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91.7%; Pred. No. 3.7e-05;
Live 1; Mismatches 0; Indels
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98SE-0002562.
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29-DEC-1998;
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                            AAY78047 standard; Peptide; 12 AA.
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91.7%;
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98SE-0004614.
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Matches 11; Conservative
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Pred. No. 3.7e-05;
1; Mismatches 0; Indels
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as can be used for treating and/or tumours. The peptides can also be used curinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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1. Similarity 91.7%; Pred, No. 4e-05;
11; Conservative 1; Mismatches 0; Indels
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AAY78037 standard; Peptide; 13 AA.
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98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                                                            bactericidal; preservative.
                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ASCI-) A+ SCI INVEST AB.
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Matches 11: Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUL-1999;
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29-DEC-1998;
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                                                                                                                                        25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
                                                                  AAY78037;
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AAY78049 standard; Peptide; 13 AA.

AAY78049;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as uninary tract infections and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                     Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; collitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolphin GT;
                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattsby-Baltzer I, Baltzer L,
                                                                                                                            AAY78048 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 15; Page 74; 102pp; English
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91.7%;
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 CFOWORNLRKVR 12
                   2 CFQWQRNMRKVR 13
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                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
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                                                                                                                            Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dolphin GT;
                                                                                                 Human lactoferrin derived peptide SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human lactoferrin derived peptide SEQ ID NO:36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 74; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                         98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                          99WO-SE01230.
                                                                 (first entry)
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                     WO200001730-A1.
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                                                                                                                                                                                                                       Homo sapiens.
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29-DEC-1998;
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                                                                   25-APR-2000
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                                                                                                                                                                                                                                       Synthetic.
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Gaps ;

0; Indels

1; Mismatches

11; Conservative

Matches

Query Match Best Local Similarity

1 CFOWORNLRKVR 12

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2 CFOWORNMRKVR 13

RESULT 7 AAY78049

Score 68; DB 21; Length 13; Pred. No. 4e-05;

WO200001730-A1

Synthetic.

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Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; uninary tract infection; collitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                               Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT,
                                                                                                                                                                                                                                                               Claim 12; Page 69; 102pp; English
                                                                                                                                        98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                       99WO-SE01230.
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                                                                                 WO200001730-A1.
                                                        Homo sapiens.
                                                                                                                      06-JUL-1999;
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                                                                Synthetic.
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also funciously and bactericidal and may also be used as preservatives. AAY78001 to AAY78100 represent peptides having sequences based on human Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

14 AA; Seguence

Gaps 6 97.1%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 4.4e-05; ive 1; Mismatches 0; Indels 11; Conservative Local Similarity Query Match Matches

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1 CFQWQRNLRKVR 12

3 CFQWQRNMRKVR 14

AAY78050 standard; Peptide; 14 AA. (first entry) 25-APR-2000 AAY78050; AAY78050 ID AAY7 RESULT 9

Human lactoferrin derived peptide SEQ ID NO:50.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

99WO-SE01230.

06-JUL-1999;

13-JAN-2000.

WO200001730-A1.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula, anti-inflammatory; anti-miorobial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                    New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                           Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                                                                                                                                        Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                    Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78051 standard; Peptide; 14 AA.
                                                                                                                                        98SE-0002562.
                                                                                             99WO-SE01230
                                                                                                                           98SE-0002441
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Matches 11; Conservative
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                                                                                             06-JUL-1999;
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                                                             13-JAN-2000
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as unfnary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                                                                                                                                                                                                                      New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide - has low toxicity, is
                                                                                                                                                                                                                          Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 75; 102pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR98554 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 11; 11pp; Japanese
                                                                                                                                                                                                                          Mattsby-Baltzer I,
                          98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                                                                          (ASCI-) A+ SCI INVEST AB
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                                                               17-JUL-1998;
29-DEC-1998;
                                 06-JUL-1998;
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AAR98554
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              The agent is low on. It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection, fungicidal; bactericidal; preservative.
                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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            AAR98531-54 are peptides used in an anti-ulcer agent. The a in toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                                   Length 15;
                                                                                                                Score 68; DB 17; Length 15
Pred. No. 4.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                       Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                       AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mattsby-Baltzer I,
                                                                                                                97.18;
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                  11; Conservative
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                                                                                                                                                                                     1 CFQWQRNLRKVR 12
                                                                                                                                                                                                                    2 CFOWORNMRKVR 13
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                                                                                                                  Query Match
Best Local Similarity
                                                                                 15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200001730-A1.
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                      AAY78035;
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15 AA;

Sequence

AAY78063 standard; Peptide; 15 AA.

RESULT 14 AAY78063 25-APR-2000 (first entry)

AAY78063;

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                                                                                                                                                                                                                                                                                                              food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                  Gaps
                                                                                                                                                                                                                                                                                                 modification; infection; inflammation; tumour;
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    Length 15;
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 Score 68; DB 21; Length 15
Pred. No. 4.7e-05;
1; Mismatches 0; Indels
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Pred. No. 4.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dolphin GT;
                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baltzer L,
                                                                                                                                                                      AAY78062 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 15; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.1%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98SE-0002441.
Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                  (first entry)
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                                                                                4 CFQWQRNMRKVR 15
                                                            1 CFOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                 Human; lactoferrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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Best Local S
Matches 11;
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                                                                                                                                                                                                     AAY78062;
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides have are also in food stuffs such as infant formula food. The peptides have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                      Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.1%; Score 68; DB 21; Length 15; 91.7%; Pred. No. 4.7e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dolphin GT;
                                                                                     Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 18; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78031 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                     98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                  99WO-SE01230,
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nes 11, Conserv
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                                                                                                                                                                                                                                                                         WO200001730-A1
                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-1998;
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Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                         Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                          Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                          Claim 11; Page 68; 102pp; English.
                                                                                                                                                                                98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                              99WO-SE01230.
       25-APR-2000 (first entry)
                                                                                                                                                                                                                      (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                            WPI; 2000-147388/13.
                                                                                                                        WO200001730-A1.
                                                                                             Homo sapiens
                                                                                                                                                              06-JUL-1999;
                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                          17-JUL-1998;
29-DEC-1998;
                                                                                                                                           13-JAN-2000
                                                                                                       Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower Sequence 16 AA;

0; Gaps 97.1%; Score 68; DB 21; Length 16; 91.7%; Pred. No. 5e-05; 0; Indels 1; Mismatches Query Match
Best Local Similarity 91.7
Matches 11; Conservative

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1 CFOWORNLRKVR 12

5 CFQWQRNMRKVR 16

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Search completed: February 21, 2003, 07:37:14 Job time : 28.35 secs

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FEATURE:
NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPOURMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-48-948-8

US-08-68-88-80-8

US-08-628-80-8

US-07-755-161A-3

US-07-755-161A-3

US-08-256-771-24

US-08-256-771-25

US-08-256-771-25

US-08-381-984-24

US-08-381-984-24

US-09-508-734-4

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-07-891-174-10

US-08-256-771-30

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-381-984-29

US-08-256-771-30

US-08-381-984-29

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US-08-381-984-29

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US-08-86-771-6

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US-08-464-182A-5
US-08-406-271-5
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                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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70
                                                                                                                                          1 CFOWORNLRKVR 12
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Match Length DB
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Perfect score:
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No.
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US-08-628-380-8
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                                          RESULT 3
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                                                                                                       Gaps
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                                                                                                                                                                                                                                                                           Sequence 8, Application US/08485948
Patent No. 2855882
GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: BUDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
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0
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0
                                                        Score 68; DB 1; Length 18;
Pred. No. 4.3e-05;
1; Mismatches 0; Indels
                                                             Length 18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 436
PRIOR APPLICATION DATA:
PUBLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATOCNEY/AGENT INFORMATION:
NAME: Jackson Beq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRN: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Klauber & Jackson
OTHER INFORMATION: (20-37) "
                                                    97.1%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                Query Match
Best Local Similarity 91.79
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                               1 CFQWQRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
    ; OTHER IN!
US-08-204-487-3
                                                                                                                                                                                                                                       RESULT 2
US-08-485-948-8
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APPLICANT: LI, YONG MING
APPLICANT: VLASSARA, HELEN
APPLICANT: VLASSARA, HELEN
APPLICANT: CERMI, ANTHONY
APPLICANT: CERMI, ANTHONY
NITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 8, Application US/08475055
Patent No. 5962245
GENERAL INFORMATION:
APPLICANT: YOUR MING LI
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97.1%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 4.3e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION NUMBER: US 08/418,642
ATTONNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1875-5800
                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Sequence 8, Application US/08628380
Patent No. 5891341
GENERAL INFORMATION:
                                                                                                                                                                                                                                   STREET: 411 Hackensack Avenue CITY: Hackensack
                                                                                                                                                                                                               ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 91.7%
.....hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FRAGMENT TYPE: internal US-08-628-380-8
                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                 STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWORNLRKVR 12
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NAME/KEY: modified site
LOCATION:
NAME/KEY: modified site
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LOCATION:
NAME/KEY: modified site
LOCATION:
LOCATION:
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LOCATION:
CTHER INFORMATION:
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LOCATION:
AUTHORS
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OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT PAPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOCUMENT NUMBER:
FILING DATE:
PRILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION;
                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE:
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VOLUME:
ISSUE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN:
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DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
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MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Jackson Esg., David A.
REGISTATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE: 09/48,217
FILING DATE: JUNE 7,1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7,1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackbon Ebg., David A.
                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/07755161A
Patent No. 5304633
                SEE: Klauber & Jackson
: 411 Hackensack Avenue
Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 18 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 97.1
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; FRAGMENT TYPE: internal US-08-475-055-8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                         New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQRNLRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                       STATE: New COUNTRY: US ZIP: 07601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-755-161A-3
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LOCATION: 19
IDEMINICATION
IDEMINICATION
IDEMINICATION
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
                                           OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cyg residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19" FFATURE: NAME/KEY: modified site LOCATION: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: TANAKA, SHGRAU
APPLICANT: TANAKA, SHGRAU
APPLICANT: TANAKA, SHGRAII
APPLICANT: KAWASAKI, YOSHININO
APPLICANT: KAWASAKI, YOSHININO
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB 1; Length 20, Pred. No. 4.8e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & SADDRESSEE: THIBBAULT STREET: 53 STATE STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPRATIE: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE TOWNER: PJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-204-487-1
; Sequence 1, Application US/08204487
; Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 97.1%;
1 Similarity 91.7%;
11; Conservative
                            IDENTIFICATION METHOD:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNLRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MA
USA
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      LOCATION:
                                                                                                                                                                                                                                                                                                                JOURNAL:
VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
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CITY: BO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                         Gaps
  Pred. No. 4.8e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                               Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDLUM TYPE: Diskette, 5.25 inch, 500Kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acid TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: DisplayWrite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: modified site
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                            1 CFQWQRNLRKVR 12
                                                                                                 2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDIVIDUAL ISOLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAPLOTYPE:
TISSUB TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM:
                                                                                                                                                                              US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY:
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us-09-743-107b-82.rai

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Gaps
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Patent No. 5656591

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                             97.1%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 4.8e-05; ive 1; Mismatches 0; Indels
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                    ; LOCATION: 1.20
; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible COMPUTER: IBM COMPUTED: COMPUTER: SEN COMPUTER: SOFTWARE: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: Unly 22, 1994
PRICAR APPLICATION: 514
PRICAR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNES: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                             single
                                                                                                                                                   MOLECULE TYPE: peptide PEATURE:
                                                                                                                                                                                             NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNLRKVR 12
                                                                                TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C. COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20005
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Gaps
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                                                                                                                                                                                                                                                                               US-08-256-771-25

Sequence 25, Application US/08256771

Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: PRODUCTS THEREWITH
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
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| IDENTIFICATION: /Note= "Cys residues are protected to
| OTHER INFORMATION: prevent disulfide bond"
| US-08-256-771-25
                                            Query Match
97.1%; Score 68; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.8e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 97.1%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.8e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: WESTINGUEN
STATE: WESTINGUEN
SIATE: U.S.A.
ZIP. 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM COMPATIBLE
OFBRATING SYSTEM: MS.DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U.5/08/256,771
FILING DATE: July 22, 1994
CTASSIFFCATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: TILING DATE:
APPLICATION NUMBER: TILING DATE:
APPLICATION NUMBER: TILING DATE:
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: TELECOMMUNICATION INFORMATION:
TELEBRONE 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                            1 CFOWORNLRKVR 12
                                                                                                                                                                                      2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWQRNLRKVR 12
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US-08-256-771-24
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TELEX:
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US-08-381-984-24
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OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment therec
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FORDER A. Application US/09508734
FORDER L. INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT APPLICATION NUMBER: PCT/KR99/00373
FRIOR APPLICATION NUMBER: KR1998-29351
FRIOR APPLICATION NUMBER: KR1998-29351
FRIOR FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
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                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
           805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                US/08/381,984
                                                                                                                                                              COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381
FILING DATE: April 11, 1995
CLASSIFICATION 25.2
PRIOR APPLICATION 25.2
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Conservative
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IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
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                                 Washington
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                                                                            U.S.A.
                                                                                                  20005
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                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97.1%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 4.8e-05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                              E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
PLIASSIFICATION: 252
PLIASSIFICATION 252
APPLICATION DATA:
APPLICATION NUMBER:
Sequence 24, Application US/08381984
Patent No. 5804555
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 25, Application US/08381984
; Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTONIEL FALLE
NAME: Warren M. Cheek, Jr.
REGIESTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 24:
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
                                                                                                                                                                                 STREET: 805 FILLE CITY: Washington
                                                                                                                                                                                                           CITI:
STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                              20005
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us-09-743-107b-82.rai

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OTHER INFORMATION: (note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" PUBLICATION INFORMATION: AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
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Best Local Similarity 91.7%; Pred. No. 6e-05;
Matches 11; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                            33,367
                                                                                             REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: modified site LOCATION: 4 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified site LOCATION: 21 IDENTIFICATION METHOD:
                                                                                                                                                            TELEFAX: 202-371-8856
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
CELL TYPE:
CELL LINE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN:
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                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

GENERAL INPERMATION:

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION: useful microorganism thereof

TITLE OF INVENTION: useful microorganism thereof

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: US/09/508,734

PRIOR APPLICATION NUMBER: KR1999-00373

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR APPLICATION NUMBER: KR1998-29351

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71
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                                                                                                                                                            0; Gaps
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                                                                                                        97.1%; Score 68; DB 4; Length 22; 91.7%; Pred. No. 5.3e-05; ative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 4; Length 24;
Pred. No. 5.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
US-07-755-161A-10
Sequence 10, Application US/07755161A
Sequence 10, Application US/07755161A
Sequence 10, Sa04633
SEGNERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Discrete, 5.25 inch, 500Kb COMPUTER: Discrete, 5.25 inch, 500Kb COMPUTER: IBM COMPACIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: DisplayWrite CURENT APPLICATION NUMBER: US/07/755,161A FILING DATE: 19910905 CLASSIFICATION: 530 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 97.1%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                     Matches 11; Conservative
                TYPE: PRT
CORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                 1 CFQWQRNLRKVR 12
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                                                                                                                                                                                                                           2 CFQWQRNMRKVR 13
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                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            RESULT 13
US-09-508-734-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
LENGTH: 24
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LENGTH: 22
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Gapa

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/note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
        Sequence 10, Application US/07891174

Patent No. 5317084

Sequence 10, Application US/07891174

Patent No. 5317084

Sequence 10, Application US/07891174

Patent No. 5317084

Sequence 10, Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSE: Wenderoth, Lind & Ponack
STREET: BO.C.

CULTY: Washington

STREET: BO.C.

COUNTER: U.S.A.

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500Kb

COMPUTER: EDISACTE: 29-MAY-1992

COMPUTER: Displaywrite

COMPUTER: Displaywrite

COMPUTER: Displaywrite

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 07/755,161

FILING DATE: 29-MAY-1992

CLASSIFICATION NUMBER: US 07/755,161

FILING DATE: 05-SER-1991

ATTORNEY/AGENT INFORMATION:

NAME: WATTEN NUMBER: 33,367

REGISTRATED NUMBER: 33,367

REGISTRATED NUMBER: 33,367

REGISTRATED NUMBER: 202-371-8856

TELEFENX: 202-371-8856
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LOCATION: 4
LDENTIFICATION METHOD:
OTHER INFORMATION: /note=
OTHER INFORMATION: Cys re
OTHER INFORMATION: thiol
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21
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SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
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CHROMOSOME/SEGMENT:
MAP POSITION:
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CELL TYPE:
CELL TYPE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: lir
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
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US-07-891-174-10
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: February 21, 2003, 07:50:36 Job time: 8.7 secs
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FILING DATE:
FUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 11; Conservat
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                                                                                                                                                JOURNAL:
VOLUME:
                                                                                                                              TITLE:
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GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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Run on:

February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec

US-09-743-107B-82 70 Perfect score:

1 CFQWQRNLRKVR 12 Sequence:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

156504 seqs, 31069816 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published Applications AA:*

1. cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USOS_PUBCOMB.pep:* /cgn2_6/ptodata//2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBGOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARTES

			Description		Semience 2 Applia	10	,	Semionos 6 Applia	2 0	, ,	Š.	sednence /, Appli	Sequence 4, Appli	Segmence 22. April	ì	· (Sequence 29, Appl	Sequence 30, Appl		Seminary 10 Seminary	רמיני שון סטמסינטסט	added to a standar	Sequence 47985, A	Seguence 4. Appli	Seminary April 4	Sequence 13026. A
SOMMAKIES			ID		US-09-798-869-2	US-09-798-869-20	US-10-023-096-2	3-8-8-8-80-SD	US-09-798-869-3	118=09=798=869=33	TIS-09-798-868-7	1-699-67-69 00	US-09-798-869-4	US-09-798-869-22	IIS-09-798-869-8	700 000 000	02-03-138-867-53	US-09-798-869-30	US-09-738-626-5715	US-09-881-579-10	75-09-881-579-15		US-08-864-761-4785	US-10-051-409-4	US-09-815-242-12129	
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10 US-09-864-761-37353 9 US-10-066-500-58 9 US-10-066-273-58 9 US-10-066-273-58 9 US-10-066-273-58 9 US-10-066-273-58 10 US-09-904-536-8 10 US-09-904-536-11 10 US-09-904-536-12 10 US-09-904-536-13 10 US-09-904-536-14 10 US-09-904-536-16 10 US-09-904-536-16 10 US-09-904-536-16 10 US-09-904-536-10 10 US-09-904-536-10	55555
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ALIGNMENTS

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Gaps
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                                                                                                                                                                            FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SVENDSEN
APPLICANT: (YSTEIN REKRAL
APPLICANT: BALDUR SVEINBJ (RNSSON)
                                      Sequence 2, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWORNLRKVR 12
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Best Local Similarity
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US-09-798-869-20
RESULT 1
US-09-798-869-2
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9-698-863-00-SD
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LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell U.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
TITLE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PC PC DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                     97.1%; Score 68; DB 9; I
91.7%; Pred. No. 4.4e-05;
tive 1; Mismatches 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY AGENT INFORMATION:
NAME: Player, William E.
REGISTRATION NUMBER: 11,409
REFERENCE/DOCKET NUMBER: 11,505/P58185C
TELECOMMUNICATION INPORMATION:
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-38
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELED FOR Windows Version 4.0
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APPLICATION NUMBER: US/10/023,096
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Patent No. US20020160941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Kruzel, Marian L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 638-6666
TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1: 694 amino acids amino acids
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Best Local Similarity 91.7
Matches 11; Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                   CRGANISM: Homo Sapiens US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 CFOWORNLRKVR 12
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US-10-023-096-2
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LENGTH: 25
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                                                         Gaps
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  97.1%; Score 68; DB 9; Length 694; 91.7%; Pred. No. 0.0011; tive 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85.7%; Score 60; DB 9; Length 15; 83.3%; Pred. No. 0.00054;
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                                                                                                                                                                                                                                                                                                                                         APPLICANT: (YSTEIN REMDAL
APPLICANT: (YSTEIN REMDAL
APPLICANT: (YSTEIN REMDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-0227
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRRENCE FOR WINDOWS VERSION 4.0
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FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1099-002-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER: OF SEQ ID NOS: 30
SEQ ID NO 3
SEQ ID NO 9
                                                                                                                                                                                                                                                                   Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
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Publication No. US20030022821A1
GENERAL INFORMATION:
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APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTEIN REXDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence
Query Match 97.1
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10; Conservative
                                                                                                     1 CFOWORNLRKVR 12
                                                                                                                                                 22 CFÓWORNMRKVR 33
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Matches 10; Conserv
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Best Local Similarity
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ORGANISM: CAPRINE
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1 CFQWQRNLRKV 11

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Gaps

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1; Indels

Mismatches

7; Conservative

Matches

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0; Gaps
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                                                                                                                                                                                        APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN RENDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OCHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVERING/RNSSON
APPLICANT: LARS VORLAND
ITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CTT/GB99/02851
PRIOR APPLICATION NUMBER: CTT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                          ; Sequence 4, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
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           3 CYÓWÓWRMRKL 13
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Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-798-869-22
                                                                                                       US-09-798-869-4
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US-09-798-869-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.4%; Score 43; DB 9; Length 15; 54.5%; Pred. No. 0.32; Live 3; Mismatches 2; Indels
                                                                                                                                               Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: CHN SIGURD SVENDEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FESEEEQ for Windows Version 4.0
SEQ ID NO 23
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APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVERNBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
FULRRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 7
SEQ ID NO 7
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Publication No. US20030022821A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
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                       3 CYQWQRRMRKL 13
1 CFOWORNLRKV 11
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Best Local Similarity
Matches 6; Conserva
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; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                            US-09-798-869-23
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Matches
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55.7%; Score 39; DB 9; Length 15; 45.5%; Pred. No. 1.4; 2; Indels tive 4; Mismatches 2; Indels
                                                               APPLICANT: CYTELN REKOLD.
APPLICANT: GYTELN REKOLD.
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTURE PEPTIDES
TITLE OF INVENTION: BIOACTURE PEPTIDES
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CPT/GB99/02851
PRIOR APPLICATION NUMBER: G99818338.4
PRIOR APPLICATION NUMBER: G99818338.4
PRIOR FILING DATE: 1998-08-31
PRIOR PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSETWARE: FastSEQ for Windows Version 4.0
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
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ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-738-626-5715
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.7%; Score 39; DB 9; Length 15; 54.5%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.7%; Score 39; DB 9; Length 15; 45.5%; Pred. No. 1.4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
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                                                                                                                                              APPLICANT: BALDUR SVEINBU (RNSSON)
APPLICANT: LARS VORLAND
TITLE OF INVENTON: BIOACTIVE PEPTIDES
TITLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1099-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-31
SOFTWARE: FASEUSEO for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: JOHN SIGUED SUNDERN
APPLICANT: JOHN SIGUED SUNDERN
APPLICANT: JOHN SIGUED SUNDERN
APPLICANT: APPLICANT: ALDUR SUEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A4649-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CFC/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GE9918938.4
PRIOR FILING DATE: 1998-08-21
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAESEQ FOR WINDGWB VERSION 4.0
                                    ; Sequence 9, Application US/09798869; Publication No. US20030022821A1; GENEAL INFORMATION:
APPLICANT: JOHN SIGHED SVENDEN; APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 45.5
Matches 5, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQRNLRKV 11
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Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-798-869-29
                 8-698-867-60-SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                         APPLICANT: OZAKT, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR PLING DATE: 1999-12-16
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR PLING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: UP 00/280988
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-06-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver: 3.0
SEQ ID NO 515
LENGTH: 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
Sequence 5715, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Corynebacterium glutamicum
                                                                                     MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
OCHIAI, KEIKO
                                                                                                                                                                             YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                              APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 54.5
Matches 6; Conservative
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73 FEYRRQLRKIR 83
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RESULT 12 US-09-798-869-30

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                                         Sequence 10, Application US/0981579;
Sequence 10, Application US/0981579;
Publication No. US2030028904A1
Senematal Involvantion:
APPLICANT: Tina L. Gumienny
APPLICANT: Annie-Carola Tosello-Trampont
APPLICANT: Jason M. Kinchen
APPLICANT: Michael O. Hengartner
APPLICANT: Michael O. Hengartner
APPLICANT: Michael O. Hengartner
TITLE OF INVENTION: Genes Involved In Engulfment of Dying
TITLE OF INVENTION: Cells and Cell Migration
FILE REFERENCE: 1314.2008-001
CURRENT PILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: 60/285,469
PRIOR FILING DATE: 2001-06-14
PRIOR FILING DATE: 2001-04-19
SOUTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 607
TYPE: PRT

ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15. Application US/09881579

Sequence 15. Application US/09881579

Publication No. US20030028904A1

GENERAL INFORMATION:

APPLICANT: Tina L. Gumienny

APPLICANT: Enrico Brugnera

APPLICANT: Annie-Carole Tosello-Trampont

APPLICANT: Michael O. Hengartner

APPLICANT: Michael O. Hengartner

APPLICANT: Michael O. Hengartner

APPLICANT: Michael O. Hengartner

APPLICANT: Codimangalam S. Ravichandran

TITLE OF INVENTION: Genes Involved In Engulfment of Dying

TITLE OF INVENTION: Gells and Cell Migration

FILE REFERENCE: 1314.2008-001

CURRENT APPLICATION NUMBER: US/09/881,579

CURRENT FILING DATE: 2001-06-14

PRIOR FILING DATE: 2001-06-14

PRIOR FILING DATE: 2001-04-19

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15

LENGTH: 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               54.3%; Score 38; DB 9; Length 607; 66.7%; Pred. No. 76; 1; Indels tive 2; Mismatches 1; Indels
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Best Local Similarity 66.//
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Matches 6; Conservative
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140 YLWQRNLRQ 148
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; ORGANISM: Murine
US-09-881-579-15
RESULT 14
US-09-881-579-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-881-579-10
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US-09-881-579-15
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Gaps

Search completed: February 21, 2003, 08:08:08 Job time: 11.55 secs

220 YLWQRNLRQ 228

2 FQWQRNLRK 10

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds

(without alignments) 120,168 Million cell updates/sec

US-09-743-107B-82 1 CFQWQRNLRKVR 12 Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

70	scription	lactotransferrin p	lactoferrin - goat	1	þę	hypothetical profe	μ	hypothetical prote		26S proteasome SU	'n	н			hypothetical prote	probable cytochrom	cytochrome P450 ho	trichohyalin like	carcinoembryonic a	hypothetical prote		a,	cysteine synthase	conserved hypothet		3-deoxy-manno-octu	histidyl-tRNA synt	hypothetical prote	probable potassium	outer capsid prote
SUMMARIES	ΙD	TEHUL	JC2323	852107	T08030	AD2346	A28438	AB0858	T28820	E90094	B60950	F90580	T19429	T22597	T22879	T00510	T00513	B85431	D33876	AH3147	H70978	G86403	T47233	C82234	I37477	D71876	F81660	T18633	m	A45687
	DB	-	~	7	ď	N	Н	7	7	C3	N	N	2	7	~	(7	7	N	7	7	7	~	N	7	N	7	7	7	2	7
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do	Query Match	97.1	72.9	9.89		0.09	0.09	58.6	58.6	57.1	57.1	55.7	55.7	54.3	54.3	54.3	54.3	54.3	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9	52.9
	Score	99	51	48	46	42	42	41	41	40	40	39	6E	38	38	38	38	38	37	37	37	37	37	37	37	37	37	37	37	37
	Result No.	7	61	ю	4	ťΩ	Q	7	æ	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27		29

A;Accession: S20841 A;Molecule type: protein A;Residues: 20-28,'X',30-31 <ST2>

hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	ribosomal protein	ribosomal protein	ribosomal protein	50S ribosomal prot	pyridoxamine 5'-ph	pyridoxamine 5'-ph	probable pyridoxam	lipopeptide antibi	interleukin-2 rece	interleukin-2 rece	hypothetical prote	3-deoxy-manno-octu
G86506	G72115	867385	T04018	A48396	AH1301	AH1673	C89895	H97451	AB2670	AG3441	S74408	JC1113	S07442	T29571	E64639
8	7	7	N	N	N	7	7	7	7	7	Ŋ	Н	Н	N	N
759	759	962	1274	9	62	62	62	206	206	208	246	275	275	361	393
52.9	52.9	52.9	52.9	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4	51.4
37	37	37	37	36	36	36	36	36	36	36	36	36	36	36	36
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A Molecule type: mRNA
A, Residues: 1-711 < CHO>
A, Cross-references: EMBL:U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237
A, Cross-references: EMBL:U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237
A, Cross-references: EMBL:U07643; NID:9467236; PIDN:AB60324.1; PID:9467237
A, Reference mumber: S11228; MUID:90384839; PMID:2402455
A, Reference mumber: S11228; MUID:90384839; PMID:2402455
A, Reference mumber: S11228
A, Rocession: S11228
A, Rocession: S11228
A, Rocession: S11228
A, Rocession: S1128
A, Rocession: S1128
A, References: EMBL:X53361; NID:934415; PIDN:CAA37914.1; PID:934416
B, Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A, Fitle: Differential molecular mechanism of the estrogen action that regulates lactofer: A, Reference number: A45401; MUID:93125571; PMID:1480183
                                                                                                                             N;Alternate names: lactoferrin
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 21-Nov-1997 #text_change 08-Dec-2000
C;Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74
R;Cho, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: $15853
A;Status: nucleic acid sequence not shown; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ristowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Blochem, J. 276, 349-355, 1991.
A;Tille: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Accession: A45401
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIP:122202)
B;Powell, M.J; Ogden, J.E.
Nucleic Acids Res. 18, 4013, 1990
A;Title: Nucleotide sequence of human lactoferrin cDNA.
A;Reference number: S10324; MUID:90326549; PMID:2374734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S10324
A;Molecule type: mRNA
A;Residues: 3-711 < POW->
A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
                                                                                                                                                                                                                                                                                                                                                                                                 A;Reference number: G06820
A;Accession: G01394
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                        lactotransferrin precursor [validated] - human
                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 20-31 <ST1>
RESULT 1
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C; Keywords: nucleotide binding; P-loop
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                                       72.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65.78;
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   Query Match
Best Local Similarity 63.0.
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                                                                                                                                                                                                                                                  38 CYOWORRMRKL 48
                                                                                                                                                                                 1 CFOWORNLRKV 11
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Best Local Similarity
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Best Local Similarity
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                                                                                                                   A;Accession: S07160
A;Molecule type: mRNA
A;Residues: 436-447, 449-711 <RAD>
A;Molecule type: mRNA
A;Residues: 436-447, 449-711 <RAD>
A;Cross-references: BMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
B;Panella, T.J.; Liu, Y.; Huang, A.T. Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A;Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A;Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A Map position: 3421-3423
C; Superfamily: transferrin; transferrin repeat homology
C; Superfamily: transferrin; transferrin iron binding; milk
C; Keywords: duplication; glycoprotein; iron binding; milk
F; 1-19 Domain: signal sequence #status predicted < SIG>
F; 20-711/Product: lactotransferrin #status experimental < MAT>
F; 21-356/Domain: transferrin repeat homology < TRH1>
F; 28-65, 29-50 Domain: transferrin repeat homology < TRH2>
F; 29-65, 39-56, 135-218, 177-193, 190-201, 251-265, 503-697, 595-609/Disulfide bonds: #status e
F; 157, 498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 368-400, 378-391, 425-706, 447-669, 479-554, 513-527, 524-537, 647-652/Disulfide bonds: #stat
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C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: UC2323
R;Le Provost, F:; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A;Reference number: UC2323; MUID:94380047; PMID:8093048
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R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
R;Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Bur. J. Blochem. 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A;Reference number: A31000; MUID:85076667; PMID:6510420
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A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-N, Note: this is the final paper in a series
R; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Eur. J. Biochem. 241, 303-308, 1996
A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinationer number: S74119; MUID:97054624; PMID:8898921
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
AjTile: Isolation of lactoferrin cDNA from a human myeloid library and expression of A,Faference number: S07160; MUID:88001.031; PMID:3477300
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A;Residues: 1-708 <LEP>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 0.00049;
1; Mismatches 0; Indels
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A;Residues: 3-701,'SWKPVN' <PAN>
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
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91.7%;
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Best Local Similarity
Matches 11; Conserv
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Jactoferrin - sheep (fragment)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
R.Oian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
B.Oochim. Biophys. Acta 123, 1995
A.Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet in A.Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet in A.Status: S2107
A.Accession: S2107
A.Accession: S2107
A.Accession: S2107
A.Molecule type: protein
A.Status: I.33 colA.
A.Molecule type: protein
A.Status: I.33 colA.
C.Superfamily: transferrin; transferrin repeat homology
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R;Mitchell, D.R.; Brown, K.S.
Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes A;Reference number: 216302; WUID:94274778; PMID:8006077
A;Accession: T08030
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C;Superfamily: dynein heavy chain, ciliary
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C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
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A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
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   DB 2; Length 708;
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                                                                        1; Indels
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Score 51; DB
Pred. No. 0.48
3; Mismatches
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Cjaccession: AB0858
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th. T; Connecton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov: A;Reference number: AB0502; PMID:11677608
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Nature 410, 1091-1096, 2001
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A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599,
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C;Genetics:
A;Gene: STY3070
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A;Molecule type: DNA
A;Residues: 1-205 <DOU>
A;Cross-references: GB:AF165818; NID:g13794510; PIDN:AAK39885.1; GSPDB:GN00150
C;Genetics:
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A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Molecule type: CRA
A,Residues: 1-92 - FAV>
A,Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A,Experimental source: strain Bristol N2; clone F07C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C'Species: Caenorhabditis elegans
C'Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
      C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
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R; Favallo, A.; Gattung, Submitted to the BMBL Data Library, March 1996
A; Description: The sequence of C. elegans cosmid F07C3.
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Pred. No. 37;
2; Mismatches
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Pred. No. 20;
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58.3%; Pred. No. 20,
0; Mismatches
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579 FQWQRSARLVK 589
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Matches 7; Conserv
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 9, 205-213, 2001
A.Tille: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A.Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lactoferrin precursor - mouse
NyAlternate names: lactotransferrin
C;Species Mus musculus (house mouse)
C;Species Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41205
C;Accession: A28438; A41205
C;Accession: A28438; A41205
C;Accession: A28438; A41205
A;Fitle: Lactotransferrin is the major estrogen inducible protein of mouse uterine secret A;Reference number: A92596; MUID:87280033; PMID:3611056
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A;Note: this species has also been called Salmonella typhi
C;Species: Nostoc sp.
A;Note: Nostoc sp.
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-201 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
R;Kaneko, T.; Nakamiya
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                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-298 <KUR>
A;Cross-references: GB:BA00019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:J03298
R;Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
J. Biol. Chem. 266, 21880-21885, 1991
J. Hicle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
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F;20-707/Product: lactotransferrin #status predicted <MAT>
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
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Pred. No. 7.7;
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0; Mismatches

7; Conservative

Matches

163 FHWORNYRK 171

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RESULT 6

2 FQWQRNLRK 10

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60.0**%**; 77.8**%**;

Query Match Best Local Similarity

A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: alr4323

A;Status: preliminary A; Accession: AD2346

A;Molecule type: DNA
A;Residues: 1-15 <LIU>
A;Cross-references: GB:M74778
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>

A; Accession: A41205

A; Molecule type: mRNA A; Residues: 3-707 < PEN>

A;Accession: A28438

2; Mismatches

6; Conservative

Matches

ð

RESULT 7

60.0**%**; 54.5**%**;

Query Match Best Local Similarity

56

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apolipoprotein B-100 - rat (fragment)

C;Accession: B60950

6; Conservative

Matches

à

Query Match Best Local Similarity

A,Gene: prsB5 A,Map position: 1 A,Genome: nucleomorph C,Keywords: nucleomorph

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A;Map position: 3
A;Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2;
                                                                           A, ALVA, C.
A, Reference number: 219123
A, Reference number: 219123
A, Accession: 119429
A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Redidues: 1-681 «MIL.
A, Redidues: 1-681 «MIL.
A, Cross-references: EMBL. 281475; PIDN: CABO3914.1; GSFDB: GN00021; CESP: C24H11.8
A, Experimental source: clone C24H11
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A;Cross-references: EMBL:Z83231; PIDN:CAB05749.1; GSPDB:GN00020; CESP:F57G9.1
A;Experimental source: clone F57G9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A;Experimental source: clone F53H4
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T22879
R;Steward, C.
Submitted to the EMBL Data Library, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
S:Dobson, R.
submitted to the EMBL Data Library, October 1996
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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A;Accession: T22879
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Molecule type: DNA
A;Residues: 1-275 <WIL>
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Best Local Similarity 60.0
Matches 6; Conservative
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A;Accession: T22597
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192 RWQKNRRRVR 201
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A;Gene: CESP:F53H4.4
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A;Gene: CESP:F57G9.1
                               C; Accession: T19429
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C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: F90580
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rilaw, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
J. Lipid Res. 31, 1109-1120, 1990
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A;Reference number: A60950; MUID:90324804; PMID:2373961
A;Accession: B60950
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A,Note: authors translated the codon ATA for residue 8 as Val
C,Superfamily: apolipoprotein B
C,Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
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A;Cross-references: GB:AL445566; PID:g14089965; PIDN:CAC13723.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
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                                                                                                                                                          Length 205;
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                                                                                                                                                       57.1%; Score 40; DB 2; 75.0%; Pred. No. 12; ive 1; Mismatches
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Conservative

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Best Local Similarity

Matches

Query Match

Conservative

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RESULT 12 T1.9429

Local Similarity

Best Loca Matches

Query Match

A; Genetic code: SGC3

A; Gene: MYPU_5500

Genetics:

A;Status: preliminary A;Molecule type: DNA

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                                             Query Match 54.3%; Score 38; DB 2; Length 357; Best Local Similarity 54.5%; Pred. No. 47; Matches 6; Conservative 5; Mismatches 0; Indels
A; Introns: 155/2; 207/3; 248/3; 290/2
                                                                                                                                               2 FOWORNLRKVR 12
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317 WKYRRNLRKIR 327

probable cytochrome P450 At2g23220 [imported] - Arabidopsis thaliana (5) Species: Arabidopsis thaliana (mouse-ear cress) (5) Species: Arabidopsis thaliana (mouse-ear cress) (5) Accession: T00510; A84622 (5) A84622 (7) A8462 (7) A8

A; Accession: T00510

A; Status: translated from GB/EMBL/DDBJ
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-515 < ROUS
A; Cross-references: EMBL: AC002391; NID: 92642427; PID: 92642441
A; Experimental source: cultivar Columbia
R; M; Kao, H; Moffat, S; Rounsley, S.D.; Ansa, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
W; Koo, H; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Bisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MUID: 20083487; PMID: 10617197

A;Accession: A84622 A;Status: preliminary A;Molecule type: DNA

4, Residues: 1-515 <STO>

A, Cross-references: GB: AE002093; NID: 92642441; PIDN: AAB87109.1; GSPDB: GN00139

C;Genetics:

A, Gene: At2g23220; T20D16.15

A;Map position: 2 A;Introns: 182/3; 310/3 C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology C;Keywords: heme; iron; metalloprotein F;312-471/Domain: cytochrome P450 homology <P45> F;449/Binding site: heme iron (Cys) (axial ligand) #status predicted

Gaps · ` Query Match 54.3%; Score 38; DB 2; Length 515; Best Local Similarity 83.3%; Pred. No. 68; Matches 5; Conservative 1; Mismatches 0; Indels

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1 CFOWOR 6 g

469 CFEWOR 474

Search completed: February 21, 2003, 07:47:54 Job time : 10.65 secs

us-09-743-107b-82.rsp

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                                                                                                       February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec
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Q14573 P
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Q04916
Q15398
Q10201
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Q99up4
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TRFL_CAPHI
DYHB_CAPHI
DYHB_CHIAR
TRFL_HORSE
TRFL_HORSE
MIA_DROME
RL2B_THETN
RA34 HUMAN
SYH_CHLMU
SYH_CHLMU
SYH_CHLMU
SYH_CHLMU
YWX7_SCHPO
RL2B_BACST
RL2B_BACST
RL2B_STAAM
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IL2A_SHEEP
SYH_CHLPN
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YEBA HAEIN
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SEQUENCE FROM N.A.
TISSUE-Mammary gland;
TGFORG H., Chen X., Huan L.;
"CDNA cloning and sequence analysis of human lactoferrin.";
submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

sequences."; Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases SEQUENCE FROM N.A. TISSUE=Prostate; Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. [8]

Tue Dec

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SEQUENCE OF 237-711 FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,

Mhan W., Parnell I., Dedhia N., Ansari A., Mardis E., Schutz K.,

Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,

Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,

Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,

Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,

Sagripanti J.L.,

Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=90064528; PubMed=258556;
Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                                                 "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of
                                                                                                                                                                                                                                                                                                                MEDLINE-82046817; Pubmed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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MEDLINE=97156796; PubMed=9003186;
Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031; PubMed=3477300;
Rado T.A., Wei X., Benz E.J. Jr. F.
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'Mutagenesis of the histidine ligand in human lactoferrin: iron
                                                                                                                                   SEQUENCE OF 20-711.

MEDLINE=85076667; PubMed=6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F., Herz-Boutigue M.-H., Wontreuil J., Jolles P.;
Hymman lactodransferrin: amino acid sequence and structural comparisons with other transferrins.";
Eur. J. Blochem. 145:659-666(1984).
                                                                                                                                                                                                                                                                                                 PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   binding properties and crystal structure of the histidine-
253-->methionine mutant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'An 88 amino acid long C-terminal sequence of human
                TISSUE=Mammary gland;
MEDILINE=90326549; PubMed=2374734;
Powell M.J., Ogden J.E.; human lactoferrin cDNA.";
"Nuclocide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                               "The present state of the human lactotransferrin
                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochim. Biophys. Acta 670:243-254 (1981)
                                                                                                 Nucleic Acids Res. 18:4013-4013(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=82262043; PubMed=7049727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 142:107-110(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                        and C-terminal domains.";
SEQUENCE OF 3-711 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 609-711.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUBLLY BICARBONATE.
FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST
LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE
                                                                                                                                                                                                   MEDLINE-91166929; PubMed=1369293;
Tani F., Ito K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
from human lactoferrin.";
                                                                                                                                                                                                                                                                                                                         Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
Hejtmancik J.F., Teng C.T.,
"Familial subepithelial corneal amyloidosis (gelatinous drop-like
corneal dystrophy): exclusion of linkage to lactoferrin gene.";
Mol. Vision 4:31-32(1998)
MHICH.
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                      Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker B.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted.
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS
                                                                               ANGSTROMS).
                                                                                                                                                                                                                                                               Agric. Biol. Chem. 54:1803-1810(1990).
                                               Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                    CHARACTERIZATION OF LACTOFERROXINS.
                                                                            X-RÀY CRYSTALLOGRAPHY (2.0 ANGSTRC
MEDLINE=99192677; PubMed=10089508;
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X52941; CAA37116.1; -.
U95626; AAB57795.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X53961; CAA37914.1; -.
EMBL; U07643; AAB60324.1; -.
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12-MAR-97.
21-APR-97.
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1LCT; 31-OCT-93
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1LFG;
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1BKA;
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1HSE;
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                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleogtomi,
Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                         STRAIN=Somali; TISSUE-Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of Camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BMBL; AJ131674; CAB53387.1; -.
BSMBL; AF165879; AAF82241.1; -.
HSSP; O77811; 1B1X.
INTEXPO; IPRO01156; Transferrin.
PFIGHTS; PRO0452; TRANSFERRIN.
SMRITS; PRO0405; TRANSFERRIN.
SMRITS; PRO0205; TRANSFERRIN.
SMRITS; PRO0205; TRANSFERRIN.
PROSITE; PRO0206; TRANSFERRIN.
PROSITE; PRO0206; TRANSFERRIN.
PROSITE; PRO0207; TRANSFERRIN.
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  Query Match

97.1%; Score 68; DB 1; Length 711;
Best Local Similarity 91.7%; Pred. No. 0.00017;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                   Camelus dromedarius (Dromedary) (Arabian camel).
                                                                                                  TRFL CAMDR STANDARD; PRT; 708 AA. O9TUMO; Q9MZS5; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update)
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LACTOTRANSFERRIN
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                                                                                                                                                 Lactotransferrin precursor (Lactoferrin).
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"Characterization of the goat lactoferrin cDNA. Assignment of the
relevant locus to bovine U12 syntemy group.",
Biochem. Biophys. Res. Commun. 2031324-1332(1994).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TYO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
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G -> A (IN REF. 2)

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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                    IRON 1 (BY SIMILARITY).
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IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
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N-LINKED (GLCNAC...)
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AC 029477; 029479;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DCO (Rel. 37, Last sequence update)
DT 15-DCO (Rel. 37, Last sequence update)
DF 15-DCO (Rel. 37, Last sequence update)
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TISSUE=Mammary gland;
MEDLINE=94380047; PubMed=8093048;
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708 AA;
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272
414
452
545
614
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4568 AA

STANDARD;

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Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                 Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonae.
                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Dynein beta chain, flagellar outer arm.
Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                   STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   NCBI_TaxID=3055;
                                                                  DYHB CHLRE
Q39565;
01-NOV-1997
01-NOV-1997
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                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                         EMBL; U53857; AAA97958.1; -.
HSSP; 077698; 1CE2.
InterPro; IPR001156; Transferrin.
PFINITS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER, 2.
PROSITE; PS00206; TRANSFERRIN.
PROSITE; PS00206; TRANSFERRIN.
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1 -> V (IN REF. 2).
2 -> K (IN REF. 2).
5 -> P (IN REF. 2).
5 -> R (IN REF. 2).
5 -> R (IN REF. 2).
6 -> G (IN REF. 2).
7 -> F2EDA3C83539960D CRC64;
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(GLCNAC. . .)
(GLCNAC. . .)
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                               LACTOTRANSFERRIN
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chain genes.";
J. Cell Sci. 107:635-644(1994).
-1- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                    DYNEIN HAS ATPASE ACTIVITY.
-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
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Interpro: IPR004273; Dynein, heavy.
Pfam; PP03028; Dynein, heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65.7%; Score 46; DB 1; Length 4568; 58.3%; Pred. No. 9; ive 2; Mismatches 3; Indel8
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ATP (POTENTIAL)
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ID TRFL HORSE STANDARD;

DT 15-JUL-1999 (Rel. 38, Created)
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143
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                                                                                                                                              resolution.";
J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                       Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                    SEQUENCE FROM N.A.

Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IRON 1 (BY SIMILARITY).
                                                                                                                                                                                            - SUBCELLUIAR LOCATION: Secreted.

- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.

- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                             LACTOTRANSFERRIN
                                                                                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                   TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
                                                                                                                                                                                                                                                                                                                                                                                                            695
695
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1179
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                               Equus caballus (Horse)
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MEDILIBE-22042099; PubMed=1939212;
Liu Y., Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Biol. Chem. 266:21880-21885 (1991).
--I- FUNCTION: TRANSPERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                              (POTENTIAL)
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Pred. No. 4.3;
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
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-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRFL MOUSE STANDARD; PRT; 707 AA. P08071; P70690; Q61799; Q922P2; 01-AUG-1988 (Rel. 08, Created) 15-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol. Chem. 262:10134-10139(1987)
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-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IISSUE=Uterus;
MEDLINE=87280033; PubMed=3611056;
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58.3%;
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Best Local Similarity
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NIA OR CG6072.

Drosophila melanogaster (Fruit fly).

Bukaryota, Matazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Bukaryota, Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

Insecta, Pterygota; Neoptera, Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)

Nebula protein.

SEQUENCE FROM N.A. McCormick A.V., Goldberg M.L.; "Gene required for elongation of meiosis I spindle in Drosophila

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

STRAIN=Berkeley; MEDLINE=20196006; PubMed=10731132;

SEQUENCE FROM N.A.

females.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                          359 S -> T (IN REF. 2).
449 A -> D (IN REF. 1).
449 E -> G (IN REF. 2).
629 L -> V (IN REF. 1).
77865 WW. P26AE0340A4C19A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                            ANION (POTENTIAL).

N-LINKED (GLCNAC. . .) (
N-LINKED (GLCNAC. . .) (
MR -> IQG (IN REF. 1).
MR -> Q (IN REF. 2).
M -> L (IN REF. 2).
S -> T (IN REF. 2).
                                                                                                                                                                                                                                                                                              BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                                                                                                                                          BY SIMILARITY.
LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.9
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42;
Pred. No.
or send an email to license@isb-sib.ch)
                                                          MGD; MGI.96837; Ltf.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00949; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
                                                                                                                                                                                                                                                                                                                                                                     ANION
                      EMBL; D88510; BAA13633.1; -.
EMBL; BC006904; AAH06904.1; -.
EMBL; M74778; AAA39427.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.0%;
54.5%;
              EMBL; J03298; AAA40525.1; -.
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707
357
707
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216
191
                                              PIR; A28438; A28438.
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707 AA;
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                                                     HSSP; P02788; 1CB6
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413
413
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SIGNAL
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Adams M.D., Celliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Leisis S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Leisis S.E., Li P.W., Hoskins R.A., Galle R.F.,
Rab Barandon R.C., Rogers Y.-H.C., Barej S.G., Champe M., Pfeiffer B.D.,
Rab Barandon R.C., Rogers Y.-H.C., Barej S.G., Champe M., Pfeiffer B.D.,
Rab Randon R.C., Rogers Y.-H.C., Half G., Nelson C.R., Miklos G.L.G.,
Rab Abril J.F., Agbayani A., An H.-J., Andrews-Pérankoch C., Bardwin D.,
Ballew R.M., Basu A., Baxendale J., Bayzaktaroglu L., Beasley E.M.,
Ballew R.M., Cawley B.C., Bouchan M.R., Bouck J., Brokstein P., Brottler B.C.,
Buckova D., Botchan M.R., Bouck J., Brokstein P., Brottler S.M.,
Burlis K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Rabeson K.Y., Benos P.V., Bernen B.P., Barnafes P.,
Rablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Rablos B., Delcher A., Howlard T.G., Ferriac S., Pleichmann W.,
Rablos B., Delcher A., Homp Z., Mays A.D., Dew I., Dietz S.M.,
Rablos B., Delcher A., Howland T.G., Ferriac S., Fleichmann W.,
Ratris N.L., Harvey D., Hernandez J.R., Houck J.,
Raberin D., Houston K.A., Howland T.G., Wein H., Ibegam C.,
Jalali M., Kalush F., Kraft C., Kravitz S., Kulp D., Lai Z.,
Rabloon B., Lei Y., Levistey A.A., Howland T.G., Morison D.L.,
Rabloon B., Neltman G.S., Pan J. Mixon K., Muzny D.M., Nelson D.L.,
Rabloon D.M., Pittman G.S., Pan J. Muzny D.M., Nelson D.L.,
Rabloon D.M., Pittman G.S., Pan J. Muzny D.M., Nelson D.L.,
Rabloon D.M., Pittman G.S., Pan S., Pollard J., Puri V., Reder E., Shen H.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., San E.,
Rab Stirskas R., Teccor C., Turner R., Ventry W., Warsper E., Shen B.,
Randor S.M., Woodage T., Worley K., Walssenbach J.,
Randor S.M., Woodage T., Wouley K.C.,
Randor S.M., Woodage T., Wouley K., Shao G., Shao G., Shao G.,
Randor S.M., Werder E., Remison G.W., Wishilams S.M., Woodage T., Wouley S.C.;
Referer S. Spradling A.C., Stapleton M., Stupski M., Shoo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE
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292 AA.

NLA DROME STANDARD; Q9XZL8; Q9V391; 30-MAY-2000 (Rel. 39, Created)

NLA DROME ID NLA D AC Q9XZL DT 30-MA

RESULT 7

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LA34 HUMAN
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10-FEB-1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RNA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                        MEDLINE=21992816; PubMed=11997336;
Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTBINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
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                                                                                                                                                                                                            Thermoanaerobacter tengcongensis.
Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
 DB 1; Length 292;
8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 38; DB 1; Length 62; Pred. No. 2.7;
                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
50S ribosomal protein L28.
RPMB OR TTE1495.
                                                                                                                                                                                                                                     Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                              62 AA.
 Score 39; DB
Pred. No. 8.9;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AE013107; AAM24713.1; -.
55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.3%;
                        6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=MB4 / JCM 11007;
                                                          ||| |: |::|
150 FQWLRSFRRLR 160
                                             2 FOWORNLRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
            Local Similarity
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27 RWKPNIRKVR 36
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                                                                                                                                                                                                                                             NCBI_TaxID=119072;
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                                                                                                                              RL28 THETN
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P41187;
Query Match
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                                                                                                                                      QBR9UI;
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                   Matches
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                                   rpoBC opercn."; submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-!-- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
Liberobacter by amplification, cloning and sequencing of the rplKAJL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit E.D., Parham P.;
"Structural diversity in the HLA-A10 family of alleles: correlations
                                                                                                                                                                                                                                     {RNA}(N).
-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                     -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (A*3401/A*3402).
MEDIINE=99056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J. Hildebrand P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HLA-A,B antigens of black populations formed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tissue Antigens 41:72-80(1993).
-!- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE IMPOUR SYSTEM.
-!- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P30453; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-CCT-2001 (Rel. 40, Last amnotation update)
HLA class I histocompatibility antigen, AW-34 (A-10) alpha chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transferase; Transcription; DNA-directed RNA polymerase.
NON TER 146 146
SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
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Pfam; PF00562; RNA pol B; 1.
PROSITE; PS01166; RNA FOL BETA; PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (A*3401/A*3402).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                          BETA' CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
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                 POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
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ID SYH. CHLMU

SYH. CHLMU

SYH. CHLMU

AC Q9PJJ9;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 37; DB 1; Length 365; Pred. No. 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                063BF63E6E6E01F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW-34 (A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FTId=VAR 004379.

K -> N (IN A*9402).

/FTId=VAR 004380.

K -> I (IN A*9402).

/FTId=VAR 004381.

P -> S (IN A*3402).

/FTId=VAR 004382.

Q -> R (IN A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR 004384.
L -> I (IN A*3402).
/FTId=VAR 004385.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I -> V (IN A*3402)
/FTId=VAR 004379.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /FTId=VAR 004383.
W -> L (IN A*3402)
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BY SIMILARITY.
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                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W -> L (IN
/FTId=VAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     365 AA; 41055 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 1.
Pfam; PF00129; MHC I; 1.
ProDom; PD000050; MHC I; 1.
SMARI; SM00407; IGG1; 1.
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Best Local Similarity 66...,
6; Conservative
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PIR; S16771; S16771.
  MICROGLOBULIN).
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SIGNAL
CHAIN
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SOLUTION STATEMENT STATEME
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                                                                                                                                                                                                                              STRAIN=MOPD / Nigg;
MEDLINB=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Esisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic Acids Res. 28:1397-1406(2000).

-!- CATALYTIC ACTIVITY: ATP + L-histidine + tRNA(His) = AMP + diphosphate + L-histidyl-tRNA(His).

-!- GUBUNIT: HOMODIMER (BY SIMILARITY).

-!- SUBGELLULAR LOCATION: Cytoplaemic.

-!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00587; FRNA-synt 2b; 1.
Pfam; PF03129; HGTP_anticodon; 1.
TIGREAMS; TIGRO0442; hiss; 1.
PROSITE; PS50862; AA, TRNA LIGASE II; 1.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDINE-3233240; PubMed-8386274; MEDILNE-3233240; PubMed-8386274; Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.; Identification and baculovirus expression of the VP4 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1994 (Rel. 29, Created)
1-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last amoration update)
01-GRI 29, Last amoration update)
01-GRI 2994 (Rel. 29, Remagglutinin) (Outer layer protein VP4).
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Viruses, dsRNA viruses, Reoviridae, Rotavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52.9%; Score 37; DB 1; Length 428; 55.6%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             428 AA; 48939 MW; 9CF859ED0E689DDF CRC64;
                                                            Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
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InterPro; IPR004154; HGTP anticodon.
InterPro; IPR004516; Hiss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002314; tRNA-synt_2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human group B rotavirus ADRV.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; 032422; 1QE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                               NCBI_TaxID=83560;
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                        HISS OR TC0830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96051387; bubMed=7584026; Nomura N., Miyajima N., Szauka T., Tanaka A., Kawarabayasi Y., Nomura N., Miyajima N., Szauka T., Tabata S.; Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.; "Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by analysis of randomly sampled cDNA clones from human immature myeloid cell line KG-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (POTENTIAL)
                   -!- SUBCELLULAR LOCATION: Outer capsid.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 37; DB 1; Length 749;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D1223527DEAE0F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 765 A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 53;
0; Mismatches
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                                                                                                                                                                                                                                                                   InterPro, IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein KIAA0008
J. Virol. 67:2730-2738(1993)
                                                                                                                                                                                                                                                  EMBL; M91434; AAA47338.1; ~.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                      29
53
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133
407
527
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TISSUE=Eye, and Lung;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         749 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 765 AA; 85668 MW; 00AFF91A02387EA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schizosaccharomyces pombe (Fission yeast).
Eukaryota, Fungi, Ascomycota, Schizosaccharomycetes,
Schizosaccharomycetales, Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C17D1.07c in chromosome II.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
or send an email to license@isb-sib.ch).
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MEDLINE=21848401; PubMed=11859360;
                                                                                EMBL; D13633; BAA02797.1; -.
EMBL; BC010658; AAH10658.1; -.
EMBL; BC016276; AAH16276.1; -.
InterPro; IPR005026; GKAP.
Pfam; PF03359; GKAP; 1.
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Q10201;
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YBX7_SCHPO
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WEDLINE=92075758; PubMed=1742360;

A KTUÉT V., KTAPU V. WITHMAIN-Liebold B.;

A KTUÉT V., KTAPU V. WITHMAIN-Liebold B.;

A TOAR Bacillus stearothermophilus ribosomes.";

Elochimie 73:855-860(1391).

C -1- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.

DR PIR; A48396; A48396.

InterPro: IPR001383; Ribosomal L28.

DR PIEM: PR00830; Ribosomal L28.

DR PIEM: PR00830; Ribosomal L28.

KW Ribosomal protein.

FT INIT MET

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SEQUENCE 60 AA; 6810 MW; ZAD9161CD60E82F4 CRC64;
                                                                                                                                                                                                                              0; Gaps
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                                                                                                                                                                                      Query Match 52.9%; Score 37; DB 1; Length 962; Best Local Similarity 66.7%; Pred. No. 69; Matches 6; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
51.4%; Score 36; DB 1; Length 60;
Best Local Similarity 66.7%; Pred. No. 5.8;
Matches 6; Conservative 2; Mismatches 1; Indels
                                                                                                                                     DOMAIN 64 170 CH.
SEQUENCE 962 AA; 112678 MW; 97FID7FD9942DEEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Bacillales; Geobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
50S ribosomal protein L28.
EMBL, AL031322, CAA20431.1, -.
InterPro, IPR001715, Calponin-like.
InterPro, IPR001048; IQ_region.
Flam, PF00612, IQ; 1.
ProDom, PD001527, CH type; 1.
SMART; SM00033, CH; T.
Hypothetical protein.
DOMAIN 64 170 CH.
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Bacillus stearothermophilus.
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P23374;
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Search completed: February 21, 2003, 07:27:57 Job time : 4.6 secs

4 WQRNLRKVR 12 |: ||:||| 27 WKANLQKVR 35

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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
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Best Local Similarity 90.9
Matches 10; Conservative
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Q77855 human immun
Q77856 human immun
Q98rr2 guillardia
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Q9nus2 homo sapien
Q8s934 diospyros k
Q8z462 salmonella
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Q38115 bacteriopha
O31090 rhizobium l
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Q8s487 zea mays (m
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Q9ucy5 homo sapien
Q9tr80 ovis aries
                                                                  February 21, 2003, 07:25:55; Search time 20.8 Seconds (without alignments) 118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                    671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Q9UCY5
Q9TR80
Q8YP77
Q38115
O31090
Q8TAX2
Q8US32
Q8US334
Q8S934
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Q77856
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Q8S487
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sp_rodent:*
sp_virus:*
sp_vortebrate:*
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sp_bacteria:*
sp_fung1:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_organelle:*
sp_phage:*
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70
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seq length: 200000000
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Match Length DB
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Perfect score:
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Maximum DB s
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Gaps

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90.0%; Score 63; DB 4; Length 711; 90.9%; Pred. No. 0.0046; ive 1; Mismatches 0; Indels

38 AA.

PRT;

PRELIMINARY;

17 39 55.7 109 15 Q9YQC1 Q9YQQ1 W19 19 39 55.7 109 15 Q9YQC1 Q9YQQ1 Q9
17 39 55.7 109 18 39 55.7 109 20 39 55.7 109 21 39 55.7 109 22 39 55.7 109 23 39 55.7 109 24 39 55.7 115 25 39 55.7 115 26 39 55.7 115 26 39 55.7 115 27 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 28 39 55.7 17 29 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 17 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 39 55.7 10 20 30 30 30 55.7 10 20 30 30 30 55.7 10 20 30 30 30 55.7 10 20 30 30 30 55.7 10 20 30 30 30 30 30 20 30 30 30 30 20 30 30 30 30 20 30 30 30 30 20 30 30 30 30 20 30 30 30 30 20 30 30 30 30 20 30 30 30 30 20 30 30 30 30 20 30 30 30 30 20 3
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                                                                                                                                               Sato 1., "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
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0
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                       84.3%; Score 59; DB 4; Length 38; 90.9%; Pred. No. 0.0011; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                 InterPro, IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAY-2000 (TTEMBLrel. 13, Last sequence update) 01-JUN-2001 (TTEMBLrel. 17, Last annotation update) Lactoferrin (Fragment).
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(TremBlrel. 20, Last sequence update)
(TremBlrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 AA.
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                                                                                                                                                                                                           seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
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                                                                                                                     MEDLINE=96081613; PubMed=8551695;
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Best Local Similarity
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                                                                                  SEQUENCE FROM N.A
                            NCBI_TaxID=9606;
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01-MAR-2002
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Nauta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.;
"Inducible gene expression mediated by a repressor-operator system
isolated from Lactococcus lactis bacteriophage rlt.";
Mol. Microbiol. 19:1331-1341(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE=96332669; PubMed=8730875; Man Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H., Venema G., Nauta A.; Wenema G., Nauta A.; "Sequence analysis and molecular characterization of the temperate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       031090;
01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 31.0 kDa protein.
Rhizobium leguminosarum (biovar viciae).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
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Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasudda M., Tabata S., "Complete genomic sequence of the filamentous nitrogen-fixing cyanobacterium Anabaena gp. strain PCC 7120.";
                                                                                                                                                                                                                                                    Score 42, DB 16; Length 298; Pred. No. 11; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=VF39;
Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N.;
Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
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Mol. Microbiol. 19:1343-1355(1996).
EMBL; U38906; AAR18704.1;
SEQUENCE 469 AA; 53160 MW; 1F8E02D4325C6BB9 CRC64;
                                                                                                                                  EMBL, AP003596, BAB'6022.1; -.
Hypothetical protein, Complete proteome.
SEQUENCE 298 AA; 34513 MW; 64036E6B52299A9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1998 (TrEMBLrel. 08,
                                                                                                              DNA Res. 8:205-213(2001).
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Conservative
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Q8S934;
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ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nagati K., Sugano S., Shiratori A., Sudo H.,
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                               Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G., Ksenzenko V.N.; Ksenzenko V.N.; Shructural and functional organization of the exopolysaccharide biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39."; Mol. Biol. (Mosk) 32:797-804(1998). EMBL, ARCO8810; AAB88891.1; -.. Hypothetical protein. SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ1175 fis, clone PLACE1007375, weakly similar to phorbol ester/diacy1glycerol-binding protein UNC-13.
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                                                                                                                                                            58.6%; Score 41; DB 2; Length 273; 70.0%; Pred. No. 16; ive 2; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
                                                                                                                                                                                                                                                                                                                      01-070-2002 (TrEMBLrel. 21, Created)
01-070-2002 (TrEMBLrel. 21, Last sequence update)
01-070N-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ11175.
Homo sapiens (Human).
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                                    MEDLINE=99113394; PubMed=9914965
                                                                                                                                                                       Local Similarity 70.0 es 7; Conservative
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Best Local Similarity
6, Conserve
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[2]
SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWORNLR 9
                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Strausberg R.;
                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                 OSTAX2
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                                                                                                                                                                                  Matches
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Q8TAX2
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Peprmatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; Ericales; Ebenaceae; Diospyros.
NCBL_TaxID=35925;
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STRAIN-CV. HIRATANENASHI;
Nakano R., Ogura E., Kubo Y., Inaba A.;
"Water stress induces ethylene biosynthesis in Japanese persimmon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58.6%; Score 41; DB 4; Length 466; 66.7%; Pred. No. 28; ive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AB073006; BAB89349.1; -. SEQUENCE 488 AA; 55238 MW; 81C38BE8F67C21AD CRC64;
                           Ninomiya K., Iwayanagi T.,
"NEDO human cDNA sequencing project.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK002031; BAA92048.1;
HSSP, P21707; 1BYN.
                                                                                                                                                                                     InterPro; IPR000008; C2.
InterPro; IPR000064; RNA_rec_mot.
Pfam; PF00168; C2; 1.
SMRNT; PR0036; C2: 2.
SMRRT; SM00239; C2: 1.
PROSITE; PS00499; C2 DOWAIN 1; UNKNOWN 1.
PROSITE; PS00049; C2 DOWAIN 2; 1.
PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
SEQUENCE 466 AA; 53192 MW; E4113A5062F58D6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TIEMBLrel. 21, Created)
01-JUN-2002 (TIEMBLrel. 21, Last sequence update)
01-JUN-2002 (TIEMBLrel. 21, Last annotation update)
1-aminocyclopropane-1-carboxylate synthase.
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
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Best Local Similarity
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SEQUENCE
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                  RESULT 12
Q77855
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           MEDLIRE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Parkhill J., Dougan G., James K.D., Thomson N.R., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                 58.6%; Score 41; DB 16; Length 511; 58.3%; Pred. No. 31;
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63.6%; Pred. No. 59;
tive 2; Mismatches 2; Indels
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EMBL, 105038; AAG24025.1; -.
InterPro; IPR000731; HMGCR/patch_5TM.
PROSITE; PS50156; SSD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The sequence of C. elegans cosmid F07C3.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;
                                                                                                                                                                                                                                                                           EMBL; AL627276; CAD06049.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 105.1 kDa protein.
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Matches 7; Conservative
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Favello A., Gattung S.;
"The sequence of C. eleg
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"Direct Submission.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               350 CFAWDMNKAKVR 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWORNLRKVR 12
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                                                                                                                                                                                                                                               MEDLINE=95191002; PubMed=7884875; Maiken C.L., Dekker J., Medler-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J., Scherpbler H.J., de Perre P., Boer K., Goudsmit J.; Scherpbler H.J., de Perre P., Boer K., Goudsmit J.; Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is unrelated to time of HIV-1 RNA positivity in the child."; J. Virol. 69:2285-2296(1995).

BMBL, 247868; AA8882.1; -.

EIMEL: 247868; AA8882.1; -.

EIMEL: 247868; AA8882.1; -.

EIMEL: 747868; AA8882.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.1%; Score 40; DB 15; Length 91; 70.0%; Pred. No. 7.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 AA; 10530 MW; BB10C62011F305D6 CRC64;
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                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                      Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus
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PRT;
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70.08;
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Matches 7; Conservative
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PRELIMINARY;
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67 QWDRTLQKVR 76

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MEDINE-21223349; PubMed=11323671;
Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T.,
Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an enslaved algal nucleus.";
Mature 410:1091-1096(2001)
EMBL; AF165818; AAK39885.1; -.
InterPro; IPR000243; Proteasome_B.
InterPro; IPR001353; Protsme_protease.
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MBDLINE=21681879; PubMed=11823852;

Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
Arlat M., Bilault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne M., Claudel Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Squier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
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Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                       57.1%; Score 40; DB 8; Length 205; 75.0%; Pred. No. 18; tive 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL646079; CAD17685.1; -.
InterPro; IRR004844; M-ppestrase.
InterPro; IPRO04844; S/T_phosphtse.
Pfam; PPG019PS; Metallophos; 1.
Plasmid; Complete proteome.
SEQUENCE 279 AA; 31541 MW; ABB38818004B2EDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                          205 AA; 22691 MW; D30F5289CBC85049 CRC64;
                                                                                                                                                                   Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia
NCBL_TaxID=55529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           03.8X5E2;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative ICC protein homolog.
ICC OR RSP0534 OR RS00414.
                                                         01-OCT-2001 (TrEMBLrel. 18, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                205 AA
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                                                                                                                                     Guillardia theta (Cryptomonas phi).
                                PRT;
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PRINTS; PR00141; PROTEASOME.
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Best Local Similarity 75.0
Matches 6; Conservative
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                              PRELIMINARY;
                                                                                                         26S proteasome SU B5.
PRSB5.
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                                                                                                                                                      Nucleomorph.
                                                                                                                                                                                                                                                                                                                                                                                             Proteasome.
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                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                             Q98RR2;
                              098RR2
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Query Match

Best Local Similarity 41.7%; Pred: No. 25;

Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 CFQWGRNLRKVR 12

Db 244 CFQWEKGTRTAK 255

Search completed: February 21, 2003, 07:44:36

Job time: 20.8 secs
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                     February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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	Description	Human lactoferrin									
	ID		AAY78038	AAY78046	AAY78047	AAY78037	AAY78048	AAY78049	AAY78036	AAY78050	AAY78051
	DB	21	21	21	21	21	21	21	21	21	21
	Length	12	12	12	12	13	13	13	14	14	14
Query	re Match Length DB I	100.0	95.8	95.8	95.8	95.8	95.8	95.8	95.8	95.8	95.8
	Score	7.1	68	69	68	68	68	68	68	68	68
Result	No.		7	m	4	Ŋ	9	7	80	σ	10

WPI; 2000-147388/13.

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ALIGNMENTS

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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                             Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                   Human lactoferrin derived peptide SEQ ID NO:83.
                     AAY78083 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                           98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                        99WO-SE01230.
                                                             25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                             WO200001730-A1.
                                                                                                                                                             Homo sapiens.
Synthetic.
                                                                                                                                                                                                                                        06-JUL-1999;
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29-DEC-1998;
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                                         AAY78083;
RESULT 1
           AAY78083
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

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                                                                                                lattoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                      AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                             0;
              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                               Length 12;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 71; DB 21;
100.0%; Pred. No. 8.3e-06;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:38.
                                                        Claim 22; Page 36; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78038 standard; Peptide; 12 AA.
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                                                                                                                                                                                                                                                                                                                                12 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                      95.8%; Score 68; DB 21; Length 12; 91.7%; Pred. No. 2.7e-05;
                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human lactoferrin derived peptide SEQ ID NO:46.
                                                                                                                                                                                                                                                1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   AAY78046 standard; Peptide; 12 AA.
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98SE-0004614.
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                                                                                                                                                                                                                                                11; Conservative
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                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                             12 AA;
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 12; Page 70; 102pp; English.

Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13.

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Page

0;

Gaps

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0; Indels

1; Mismatches

11; Conservative

Matches

Local Similarity

Query Match

12 AA;

Sequence

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95.8%; Score 68; DB 21; Length 12; 91.7%; Pred. No. 2.7e-05;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower cannot be used for the same purposes as lactoferrin at lower
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fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                                                                   Length 12;
                                                                                                                                                                                 Score 68; DB 21; Length 12
Pred. No. 2.7e-05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:47.
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                                                                                                                                                                                                                                                                                                                                                                                AAY78047 standard; Peptide; 12 AA.
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98SE-0004614.
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                     1 CFOWORNMKKVR 12
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Best Local Similarity
Matches 11; Conserv
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through peptide are taken up in the intestine through peptide lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammantions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and a contact of the costs. Therefore is a me purposes as lactoferrin at lower and a contact of the costs.
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dolphin GT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:37.
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                                                                                                                     AAY78037 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 70; 102pp; English.
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                                                                                                                                                                                                                                                                                                                 bactericidal; preservative.
                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 91.7
Matches 11, Conservative
1 CFQWQRNIMKKVR 12
                               1 CPOWORNWRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-JUL-1999;
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29-DEC-1998;
                                                                                                                                                                                        25-APR-2000
                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                      AAY78037;
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                                                                                                  RESULT 5
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A.

AAY78049 standard; Peptide; 13

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                          Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.8%; Score 68; DB 21; Length 13; 91.7%; Pred. No. 3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dolphin GT;
                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 15; Page 74; 102pp; English.
                                                                                        AAY78048 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB.
     2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-147388/13.
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                                                                                                                                                             25-APR-2000
                                                                                                                                                                                                                                                                                                                      sapiens.
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                                                                                                                                                                                                                                                                                                                                     Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such and actoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower mable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                              Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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Pred. No. 3e-05;
1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                   Human lactoferrin derived peptide SEQ ID NO:49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 18; Page 74; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanson LA, Mattsby-Baltzer I,
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                                                                                                                                                                                                                                                                                                                                                                                98SE-0002441.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13 AA;
                                                                                                                                                                                                                                                                         WO200001730-A1.
                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                              06-JUL-1999;
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                                                               25-APR-2000
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                                                                                                                                                                                                                                         Synthetic.
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Gaps

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0; Indels

1; Mismatches

11; Conservative

Best Local Similarity

Matches

RESULT 7

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an infant lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower mable them to be used for the same purposes as lactoferrin at lower
               Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                        98SE-0002441.
                                                                                                                                                                                                                                                                                                                                            98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                               99WO-SE01230.
                                                                                   bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                           (ASCI-) A+ SCI INVEST AB
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                                                                                                                                                                                          WO200001730-A1
                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                               06-JUL-1999;
                                                                                                                                                                                                                                                                                                                      06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                              17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                     13-JAN-2000
                                                                                                                                                    Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through blinding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for tracting and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 15; Page 75; 102pp; English.

Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13

(ASCI-) A+ SCI INVEST AB.

98SE-0002441. 98SE-0002562. 98SE-0004614.

17-JUL-1998; 29-DEC-1998;

06-JUL-1998;

99WO-SE01230

06-JUL-1999;

13-JAN-2000

WO200001730-A1

Synthetic.

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                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:50.
                                                                                                                                                                                                                                                                                                                                                   AAY78050 standard; Peptide; 14 AA.
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                                                                                                                                                                       12
                                                                                                                                                                                                                     3 CFOWORNMRKVR 14
                                                                                                                                                                       CFOWORNMKKVR
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RESULT 9 AAY78050

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bactericidal; preservative

Homo sapiens

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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 3.2e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 CFOWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     14 AA;
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Synthetic.
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                                                                                                                                                         AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A madicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                   Even though mative human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                            Score 68; DB 21; Length 14;
Pred. No. 3.2e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                     Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - has low toxicity, is
                                                                     Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR98554 standard; Peptide; 15 AA.
                                                                                                                                          Claim 18; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MORG ) MORINAGA MILK IND CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-ulcer agent contg. peptide
        98SE-0002441.
98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide for anti-ulcer agent.
                                                                                                                                                                                                                                                                                                                                              95.8%;
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                 (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                        3 CFOWORNMRKVR 14
                                                                                        WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                   17-JUL-1998;
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                                                                      Hanson LA,
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would contable them to be used for the same purposes as lactoferrin at lower
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agent is low It can be
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                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                   0;
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   AAR98531-54 are peptides used in an anti-ulcer agent. The agin toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                                                                                                                     Length 15;
                                                                                                                                                                                           Score 68; DB 17; Length 15
Pred. No. 3.5e-05;
1; Mismatches. 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY78035 standard; Peptide; 15 AA.
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91.7%;
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                       2 CFOWORNMRKVR
                                                                                                                                          15 AA;
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15 AA;

us-09-743-107b-83.rag

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also infungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                  Human, lactoferrin, modification, infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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Pred. No. 3.5e-05;
1; Mismatches 0;
                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:63.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 18; Page 81; 102pp; English.
                                                                                                            AAY78063 standard; Peptide; 15 AA.
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98SE-0002562.
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Best Local Similarity
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                    Score 68; DB 21; Length 15;
Pred. No. 3.5e-05;
1; Mismatches 0; Indels
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98SE-0002562.
98SE-0004614.
                       95.8%;
91.7%;
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29-DEC-1998;
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13-JAN-2000

Synthetic.

AAY78062;

RESULT 13 AAY78062

8 요 Hanson LA,

Dolphin GT;

0;

Gaps

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Sequence

Query Match

Matches

Length 15; 0; Indels

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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                        Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                         Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                     Claim 11; Page 68; 102pp; English.
         25-APR-2000 (first entry)
                                                                                                                                                                                                        (ASCI-) A+ SCI INVEST AB.
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                                                                                                               WO200001730-A1.
                                                                                       Homo sapiens.
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29-DEC-1998;
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                                                                                               Synthetic.
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98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

Dolphin GT;

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an infant and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower

16 AA;

Gaps ; 0 95.8%; Score 68; DB 21; Length 16; 91.7%; Pred. No. 3.7e-05; tive 1; Mismatches 0; Indels Best Local Similarity 91.7 Matches 11; Conservative Query Match

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1 CFQWQRNMKKVR 12

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Search completed: February 21, 2003, 07:37:14 Job time : 28.35 secs

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NAME/KEY: Peptide
LOCATION: 1.18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 aming acids
                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
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                                                                               February 21, 2003, 07:25:59; Search time 8.65 Seconds (without alignments) 40.818 Million cell updates/sec
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/cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-204-487-1
US-08-256-771-24
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US-09-017-043A-3
US-08-464-182A-5
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                                                                                                                                                                                                                                            262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       OM protein - protein search, using sw model
                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                       Issued Patents AA:*
                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                        US-09-743-107B-83
                                                                                                                                                                      1 CFQWQRNMKKVR 12
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Query
Match Length DB
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                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                        Sequence:
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Result

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Appli
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCH, WATRU
APPLICANT: MOSUCH, WATRU
APPLICANT: MOSUCH, WATRU
APPLICANT: TANAKA, SHUN'ICHI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: CAWASAKI, YOSHIHIRO
APPLICANT: UCHIDA, TOSHIMIRO
APPLICANT: UCHIDA, TOSHIMIRO
APPLICANT: INTINION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: DEP C Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: PATENT ADMINISTRATOR, TESTA, HURWITZ
E: THIBEAULT
53 STATE STREET
US-08-464-182A-2
US-08-406-271-2
US-09-724-586-2
US-09-421-632-2
US-09-932-190-2
US-09-932-190-2
US-08-655-640-4
US-08-655-640-4
US-08-154-1019-4
US-08-464-167-4
US-08-466-1333-4
US-08-466-1333-4
US-08-466-1333-2
US-08-456-108-2
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                õ
                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-628-380-8
                                                         US-08-628-380-8
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                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
APPLICANT: ATTHONY CESAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: BUDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                         95.8%; Score 68; DB 1; Length 18; 91.7%; Pred. No. 2.2e-05;
                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:

CLASSIFICATION: 436

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: JUNE 7, 1995
CLASSIFICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION TOWNER: 26,742
ATTORNEY AND TOWNEY TOWNER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  ; Sequence 8, Application US/08485948
; Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klauber & Jackson
OTHER INFORMATION: (20-37)"
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DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 18 amino acids
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                                                                                                 Matches 11; Conservative
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FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWORNMKKVR 12
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STATE: New Jersey
                                                                                                                                         1 CFOWORNMKKVR 12
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                                                                              Best Local Similarity
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US-08-204-487-3
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US-08-485-948-8
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                                                           Query Match
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1 CFQWQRNMRKVR 12

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OPERATING SYSTEM: MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
MAMORU TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wendercth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITT: Washington
STREET: D.C.
                                                                                                                                       COMPUTER TRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/475,055
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/489,217
FILING DATE: 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY, ARBNI TINFORMATION:
NAME: JACKSON ESQ. DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECHONE: 201 487-5800
TELECHONE: 201 343-1684
TELECHONE: 13351
INFORMATION FOR SEQ ID NO: 8:
SEDUENCE CHARACTERISTICS:
TELECHONE: 13351
TELECHONE: 13351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/07755161A Patent No. 5304633
                   ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8
CORRESPONDENCE ADDRESS
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US-07-755-161A-3
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: OF Residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                      NAME: Warren M. Cheek Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELECOMMUNICATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 19
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEVELOPMENTAL STAGE:
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CLONE:
CHOMOSOME/SEGMENT:
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INDIVIDUAL ISOLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 1:
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-755-161A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VOLUME:
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DB 1; Length 20;

95.8%; Score 68;

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NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 95.8%; Score 68; DB 1; I Best Local Similarity 91.7%; Pred. No. 2.5e-05; Matches 11; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/204,487
02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:

FUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-204-487-1; Sequence 1, Application US/08204487; Patent No. 5565425; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F: 53 STATE STREET
BOSTON
                      IDENTIFICATION METHOD:
OTHER INFORMATION: /nc
OTHER INFORMATION: Cyt
OTHER INFORMATION: thi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWQRNMKKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 02
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02109
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STREET: 53
CITY: BOST
                                                                                                                                                                                                                                                                                              JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
                          ô
                          Gaps
                          0;
  91.7%; Pred. No. 2.5e-05;
cive 1; Mismatches 0; Indels
                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                    E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: IRW Compatible
OPERATING SYSTEM: Ms-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Displaykrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 05/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek JF.
RESISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                           ; Sequence 3, Application US/07891174; Patent No. 5317084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAME/KEY: modified site
                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                          1 CFQWQRNMKKVR 12
                                                                                                2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                    STREET: 805 Fifte
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 20005
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                                                                                                                                                       RESULT 6
US-07-891-174-3
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FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: Cyg residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS.
/note= "thiol group of Cys residue at location 2 connected by disulfide bond with thiol group of Cys residue at location 19"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: MOSUCHI, WATARU
APPLICANT: MOSUCHI, WATERI
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
APPLICANT: KAWASAKI, YOSHIHIRO
TITLE OF INVENTION: ULRAL INPECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
RECISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
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us-09-743-107b-83.rai

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FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                          1 CFOWORNMKKVR 12
                                                                                                                                               2 CFQWQRNMRKVR 13
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                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C. COUNTRY: U.S.A.
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      US-08-256-771-24
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US-08-381-984-24
                                             Query Match
                                                                                   Matches
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Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                            NAME/KEY: Peptide
LOCATION: 1..20
OTHER INPORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: JULY 22, 1994
PRIOR APPLICATION 1514
PRIOR APPLICATION 1514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
RILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
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NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                            20 amino acids
                                                                                                                                                                                                                                                                                                                                           11; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
                                                                             TYPE: amino acid
STRANDEDNESS: single
                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                       2 CFQWQRNMRKVR 13
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20005
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Matches 11; Conserv
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STATE: D.C.
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TELEX:
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                                                        LENGTH:
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Sequence 25, Application US/08256771
Patent No. 5565510
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION: PRODUCTS THEREWITH
TITLE OF INVENTION:
TITLE OF INV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 2.5e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUDRESSEE: Menderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STREE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: UJY 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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Patent No. 6423509

TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: useful microorganism thereof

FILE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT PILING DATE: 1999-07-14

PRIOR APPLICATION NUMBER: KR1998-29351

PRIOR FILING DATE: 1998-07-13

PRIOR FILING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: /note= "cysteine residues at positions 2 OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 2.5e-05; Live 1; Mismatches 0; Indels
                                                                                           ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
  805 Fifteenth Street, N.W., #700
                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOG
SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION:
IDENTIFICATION METHOD:
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IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWORNMKKVR 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                           Washington
                                                                          U.S.A.
                                                   STATE: D.C
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US-09-508-734-4
                                                                          COUNTRY:
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LIDBNITEICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment therec
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OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95.8%; Score 68; DB 1; Length 20; 91.7%; Pred. No. 2.5e-05; vative 1; Mismatches 0; Indels
Patent No. 5804555;
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER COF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION: 252
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
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IRY: U.S.A.
20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-381-984-24
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NAME/KEY:
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INENTIFICATION: 4
IDENTIFICATION: 4
IDENTIFICATION: 4
IDENTIFICATION: 4
IDENTIFICATION: // note= "thiol group of OTHER INFORMATION: // note= "thiol group of OTHER INFORMATION: // note= "thiol group of Cys residue at location 21"
COTHER INFORMATION: thiol group of Cys residue at location 21"
IDENTIFICATION: 21
IDENTIFICATION: 7
IDENTIFICATION: 7
IDENTIFICATION: OF SESSION OF CYS RESIDUE AT LOCATION: OTHER INFORMATION: // note= "thiol group of OTHER INFORMATION: // note= "thiol group of OTHER INFORMATION: // note = "thiol group of Cys residue at location 4"
AUTHER INFORMATION: A location of Cys residue at location 4"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,387
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 10:
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UNITS:
FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
FRAGMENT TYPE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CELL TYPE:
CELL LINE:
ORGANIELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
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HAPLOTYPE:
TISSUE TYPE:
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INDIVIDUAL ISOLATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-755-161A-10
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PAGES:
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                                                                                                                                                                                                                                                                                                                                          Sequence Application US/09508734
Facent No. 6423509
GENERAL INFORMATION:
APPLICANT: Samyang Genex Corporation
ITILE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
ITILE OF INVENTION: Useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 1099-00-14
PRIOR APPLICATION NUMBER: RR.98-29351
PRIOR FILING DATE: 1998-07-13
PRIOR FILING DATE: 1998-07-13
SOFTWARE: KOPACHOLING DATE: 1998-07-13
SOFTWARE: KOPACHOLING DATE: 1998-07-13
SEQ ID NO 6
LENGTH: 24
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95.8%; Score 68; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 3e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                            95.8%; Score 68; DB 4; Length 22; 91.7%; Pred. No. 2.7e-05; tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-07-75-161A-10

Sequence 10, Application US/07755161A

Sequence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Agent

TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPEDNUE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: Weahington

CITY: Weahington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE:

STATE:
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READBALE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
TT.ING DATE: 19910905
                                                                                                       Query Match 95.8
Best Local Similarity 91.7
Matches 11, Conservative
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
LENGTH: 22
TYPE: PRT
ORGANISM: Homo mapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                 1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                             2 CFÓWORNMRKVR 13
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STATE: D.
COUNTRY:
                                                                  US-09-508-734-4
                                                                                                                                                                                                                                                                                                                RESULT 13
US-09-508-734-6
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Gaps . 0

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OTHER INFORMATION: /note= "thiol group of CTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with CTHER INFORMATION: thiol group of Cys residue at location 4" AUTHORS AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                        Query Match 95.8%; Score 68; DB 1; Length 25; Best Local Similarity 91.7%; Pred. No. 3.1e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 21, 2003, 07:50:36 Job time : 8.7 secs
                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFOWORNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                     DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                       US-07-891-174-10
                                                                                                                          TITLE:
JOURNAL:
                                                                                                                                                                  VOLUME:
ISSUE:
PAGES:
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LOCATION: 4
LOCATION: 4
LOCATION: 4
COTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: (ys residue at location 4 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 21"
                                       Sequence 10, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                 SCHWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION NAM:
FILING DATE: 007/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 33,367
REGISTRATION NUMBER: 202-371-8850
FILIEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             modified site
21
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LENGTH: 25 amino acids
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STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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TISSUE TYPE:
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LOCATION:
  RESULT 15
US-07-891-174-10
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February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec
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2: /cgn2 6/ptodata/2/pubpaa/USOB NEW PUB.pep:*

3: /cgn2 6/ptodata/2/pubpaa/PGOF NEW PUB.pep:*

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6: /cgn2 6/ptodata/2/pubpaa/USOF NEW PUB.pep:*

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2. Appli	20.	2.	9	m	23,		30	7	4	22		113	119,	119	119.	1	14.	Sequence 6, Appli
A	US-09-798-869-2	US-09-798-869-20	US-10-023-096-2	0S-09-798-869-6	US-09-798-869-3	US-09-798-869-23	US-09-798-869-29	US-09-798-869-30	US-09-798-869-7	US-09-798-869-4	US-09-798-869-22	US-09-798-869-8	US-09-978-295A-119	US-09-978-697-119	US-09-978-192A-119	US-09-999-832A-119	US-09-978-189-119	US-09-796-753-14	US-09-981-649A-6
DB	6	σ	σ	o,	σ	σ	σ	σ	σ	0	σ	σ	Q	σ	σ	σ	σ	σ	10
* Query Match Length	15	25	694	15	15	25	15	15	15	15	25	15	338	338	338	338	338	553	553
* Query Match	95.8	95.8	95.8	84.5	71.8	71.8	63.4	63.4	9.09	59.5	59.5	54.9	54.9	54.9	54.9	54.9	54.9	54.9	54.9
Score	89	68	99	9	51	21	45	45	43	42	42	39	39	39	39	39	39	39	39
Result No.		7	m	4	D.	9	7	60	6	10	11	12	13	14	15	16	17	18	19

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10 US-09-981-649A-24 10 US-09-981-649A-30 10 US-09-981-649A-32 10 US-09-981-649A-28	9 US-09-796-753-26 10 US-09-864-761-47985 9 US-09-798-869-26 9 US-09-798-869-25 9 US-09-798-869-1	9 US-09-798-869-10 9 US-09-798-869-28 9 US-09-798-869-24 9 US-09-798-869-21	99	10 US-09-864-761-40332 9 US-09-796-692-1487 9 US-09-888-320-2 10 US-09-815-242-12129 110 US-09-815-242-13026	10 US-09-764-864-1031 10 US-09-853-625B-16 9 US-10-066-500-58
55 54 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	333 21 114 144	12 13 13 13 13 13 13 13 13 13 13 13 13 13	22 25 34 46 34 46	61 489 62 62	95 351 747
0.0000 44446 0.000	52.1 50.7 50.7	50.7 50.7 50.7 50.7	50.7 50.7 50.7 50.7	44444 00000000000000000000000000000000	47.9 47.9
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                                                                                 APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: ALDUR SVENDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BARG VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-UGA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELSEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 20, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
              Sequence 2, Application US/08798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: HOMO SAPIENS
US-09-798-869-2
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Best Local Similarity
Matches 11; Conserv
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US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 2
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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APPLICANT: Kruzel, Marian L.
APPLICANT: Kurecki, Tomasz.
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                     95.8%; Score 68; DB 9; Length 25; 91.7%; Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C.
                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
         FILE REFERENCE: A34049-PCT-USA-A
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10505/P58185C
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PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US/08/124,586
APPLICATION NUMBER: US/08/124,586
FILING DATE: 05-MAY-1394
ATTOCNEY/AGENT INFORMATION:
NAME: Player, William E.
REGISTAATION NUMBER: 1,409
REPERBNCE/DOCKET NUMBER: 1,505/P5818:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEPHONE: (202) 638-6666
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 694 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
LARS VORLAND
                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWORNMKKVR 12
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Best Local Similarity
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                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                Gaps
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US-09-798-869-6
                                                0:
95.8%; Score 68; DB 9; Length 694; 91.7%; Pred. No. 0.00088; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 60; DB 9; Length 15;
Pred. No. 0.00051;
1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: A34040-PCT-USA-A
FILE REFERENCE: A34040-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1990-08-13
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: BCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER: OF SEQ ID NOS: 30
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: BALDUR SVENDAL
APPLICANT: BALDUR SVENDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCES: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798, 869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CFG899/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
                                                                                                                                                                                                                                                 Sequence 6, Application US/09798869; Publication No. USZ0030022821A1; GENERAL INFORMATION: APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: GYSTERN REKDAL; APPLICANT: BALDUR SVEINBJ(RNSSON APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09798869 Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                83.3%;
Query Match
Best Local Similarity 91.77
Matches 11; Conservative
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                                                                                         1 CFQWQRNMKKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CPQWQRNMKKVR 12
                                                                                                                                     22 CFOWORNMRKVR 33
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Best Local Similarity
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Best Local Similarity
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; ORGANISM: CAPRINE
US-09-798-869-3
                                                                                                                                                                                                           RESULT 4
US-09-798-869-6
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US-09-798-869-3
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Matches

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1 CFQWQRNMKKV 11
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                                                                                                                                                                                                                                                                                                                              , ORGANISM: BOVINE
US-09-798-869-30
                                          US-09-798-869-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                     71.8%; Score 51; DB 9; Length 25; 63.6%; Pred. No. 0.024; ive 3; Mismatches 1; Indels
  Indels
  1,
 3; Mismatches
                                                                                                              GENERAL INDRIVATION:
GENERAL INDRIVATION:
APPLICANT: JOHN SIGRED SVENDSEN
APPLICANT: JOHN SIGRED SVENDSEN
APPLICANT: GENERAL INSERDAL
APPLICANT: BALDUR SVEINBG (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 29, Application US/09798869
; Publication No. US20030022821A1
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Matches 7; Conservative
7; Conservative
                          1 CFQWQRNMKKV 11
                                                    3 CYOWORRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWQRNMKKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 CYÓWÓRRMRKL 13
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                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: BOVINE
                                                                                                        -09-798-869-23
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54.5%; Pred. No. 0.31;
tive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEN REKDAL
THERE OF INVENTION: BLOACTIVE PEPTIDES
TITLE OF INVENTION: BLOACTIVE PEPTIDES
TITLE OF INVENTION: BLOACTIVE PEPTIDES
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
PRIOR APPLICATION NUMBER: CORP.
PRIOR APPLICATION NUMBER: CB9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASISEQ for Windows Version 4.0
                                                                 APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: HALDUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCE: A3464-PCT-USA-A
CURRENT PELLICATION NUMBER: US/09/798,869
CURRENT PELLING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: G89918938.4
PRIOR FILLING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENCTH: 15
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
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; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63.6%;
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Best Local Similarity 63.00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 54.53
Matches 6; Conservative
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File REFERENCE: P263091C11
CURRENT APPLICATION NUMBER: U5/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%; Score 39; DB 9; Length 15; 54.5%; Pred. No. 1.4; ive 2; Mismatches 3; Indels
                                                      APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798, 869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NOS: 30
SEQ ID NOS: 30
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Godowski, Paul J.
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 119, Application US/09978295A Patent No. US20020156006A1 GENERAL INFORMATION:
                  (YSTEIN REKDAL
BALDUR SVEINBJ (RNSSON
LARS VORLAND
APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pan, James;
Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferrara, Napoleon
Filvaroff, Ellen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerritsen, Mary E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerber, Hanspeter
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Botstein, David
Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 54.5
Matches 6; Conservative
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Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Ashkenazi, Avi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWQRNMKKV 11
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                  APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                 APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYGINDAL
APPLICANT: BALDUR SYGINDAL
APPLICANT: BALDUR SYGINDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOGACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02651
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELSEQ for Windows Version 4.0
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APPLICANT: (YSTEIN REKDAL
APPLICANT: BALUNK SVEINBJ(RNSSON
APPLICANT: BALUNK SVEINBJ(RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CG991838.4
PRIOR APPLICATION NUMBER: GB9818938.4
FRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 22, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
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                                ; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; Publication No. US20030022821A1
; APPLICANT: JOHN SIGURD SVENDSEN
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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ORGANISM: MURINE
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US-09-798-869-22
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US-09-798-869-8
           US-09-798-869-4
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION WUMBER: 60/081919
PRIOR APPLICATION WUMBER: 60/081952
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PRIOR APPLICATION WUMBER: 60/081952
PRIOR FILING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-15
PRIOR PRILICATION WUMBER: 60/08269
PRIOR PLING DATE: 1998-04-21
PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-29
PRIOR PRIOR DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-07
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APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Tumas, Daniel
APPLICANT: Tumas, Daniel
APPLICANT: Williams P. Mickey
APPLICANT: William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPERIOR: 105/09/978,697
CURRENT APPLICATION NUMBER: 2001-10-16
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               PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR PLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR PLING DATE: 1998-05-15
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Gerritsen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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PRIOR PILLING DATE: 1997-110-17
PRIOR FILLING DATE: 1997-110-03
PRIOR FILLING DATE: 1997-11-03
PRIOR FILLING DATE: 1997-11-13
PRIOR PELICATION NUMBER: 60/065311
PRIOR FILLING DATE: 1997-11-12
PRIOR PILLING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/067450
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: Sequence 119, Application US/09978697

: Patent No. US20020169284A1

: GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
APPLICATION NUMBER: 60/085582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Paoni, Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWQRNMKKV 11
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R. AFFLICATION NUMBER: 00/079094

R. APPLICATION NUMBER: 60/079689

R. FILING DATE: 1998-03-27

R. APPLICATION NUMBER: 60/079663

R. APPLICATION NUMBER: 60/079786

R. APPLICATION NUMBER: 60/079786
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R APPLICATION NUMBER: 60/079923

R APPLICATION NUMBER: 60/080105

R APPLICATION NUMBER: 60/080105

R FILING DATE: 1998-03-31

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R APPLICATION NUMBER: 60/080327
RR APPLICATION NUMBER: 60/080328
R FILING DATE: 1998-04-01
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R APPLICATION NUMBER: 60/081195
R FILING DATE: 1998-04-08
R FILING DATE: 1998-04-09
R FILING DATE: 1998-04-09
R APPLICATION NUMBER: 60/081203
FILING DATE: 1998-03-10
APPLICATION NUMBER: 60/077632
FILING DATE: 1998-03-11
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APPLICATION NUMBER: 60/077649
FILING DATE: 1998-03-11
APPLICATION NUMBER: 60/07791
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APPLICATION NUMBER: 60/078004
FILING DATE: 1998-03-13
APPLICATION NUMBER: 60/07886
FILING DATE: 1998-03-20
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APPLICATION UNDBER: 60/078910
APPLICATION UNDBER: 60/078939
APPLICATION NUMBER: 60/078939
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APPLICATION WINBER: 60/079656
FILING DATE: 1998-03-26
APPLICATION NUMBER: 60/079664
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APPLICATION UNDRER: 60/081070
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081952
FILING DATE: 1998-04-15
                                                                                                                                                     APPLICATION NUMBER: 60/077641
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APPLICATION NUMBER: 60/079294
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APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/080194
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R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084441
R FILING DATE: 1998-05-06
R APPLICATION NUMBER: 60/084637
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084639
R FILING DATE: 1998-05-07
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A PAPLICATION NUMBER: 60/084598
R FILING DATE: 1998-05-07
R APPLICATION NUMBER: 60/084600
R FILING DATE: 1998-5-07
                   FILING DATE: 1998-04-15
APPLICATION UNDHER: 60/082568
APPLICATION DATE: 1998-04-21
APPLICATION NUMBER: 60/082569
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APPLICATION NUMBER: 60/082804
FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082700
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
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APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/083495
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APPLICATION NUMBER: 60/083545
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/081838
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APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/083496
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558
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APPLICATION NUMBER: 60/083559
FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/083742
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FILING DATE: 1998-05-05
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FILING DATE: 1998-05-06
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/085339
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APPLICATION NUMBER: 60/085689
FILING DATE: 1998-05-15
APPLICATION NUMBER: 60/085579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/084627
FILING DATE: 1998-05-07
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FILING DATE: 1998-05-13
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APPLICATION NUMBER: 60/085700
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LING DATE: 1998-04-30
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                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                        h Similarity 54.9%; Score 39; DB 9; Length 338; Similarity 54.5%; Pred. No. 26; 6; Conservative 2; Mismatches 3; Indels
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085580
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 119, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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PRIOR PELING DATE: 1997-11-13
PRIOR PELING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILLING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/07763
PRIOR PILLING DATE: 1998-03-11
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ferrara, Napoles,
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
Goddard, Audrey
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Eaton, Dan
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Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: P2630P1C9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pan, James;
                                                                                                                                                                                                                                                                                                   1 CFOWORNMKKV 11
                                                                                                                                                                                                                                                                                                                                            50 CYGWRRNSKGV 60
                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
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US-09-978-192A-119
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NUMBER: 60/077791 1998-03-12 NUMBER: 60/078004 1998-03-13 NUMBER: 60/078886 1998-03-20 NUMBER: 60/078936 1998-03-20 1998-03-20 NUMBER: 60/078910 1998-03-20 NUMBER: 60/078910 1998-03-20 NUMBER: 60/078910 NUMBER: 60/078910 NUMBER: 60/078910	1 1998 - 03 - 03 - 03 - 03 - 03 - 03 - 03 - 0	NUMBER: 60/080333 1998-04-01 1998-04-01 1998-04-01 1998-04-01 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-08 1998-04-09 1998-04-15
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PRIOR FILING DATE: 1998-04-22
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PRIOR APPLICATION NUMBER: 60/082705
PRIOR APPLICATION NUMBER: 60/082705
PRIOR PELING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-05
PRIOR PLING DATE: 1998-05-05
PRIOR PLING DATE: 1998-05-05
PRIOR PLING DATE: 1998-05-05
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-16
PRIOR PLING DATE: 1998-

; PRIOR APPLICATION NUMBER: 60/085697

0; Gaps Query Match 54.9%; Score 39; DB 9; Length 338; Best Local Similarity 54.5%; Pred. No. 26; Matches 6; Conservative 2; Mismatches 3; Indels

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1 CFQWQRNMKKV 11 |: |: || || 50 CYGWRRNSKGV 60 à

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Search completed: February 21, 2003, 08:08:08 Job time : 10.55 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-83 71 1 CFQWQRNMKKVR 12 Perfect score: Title:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		d			SUMMARIES	
Result No.	Score	Query Match	Length	DB	Α	Description
п	689	95.8	711	ļ	TFHUL	- HILL TOTOL
2	51	71.8	708	7	JC2323	actoferrin -
m	48		33	7	0	lactoferrin - shee
4	42	59.2	511	7	AB0858	<u>-</u> ح
ιΩ	42		707	-	_	٦
9	41		282	~	F90580	_
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œ	40	56.3	275	Н	JC1113	ukin
σ	40		275	Н	S07442	N
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	39	54.9	205	7	CD.	- 5
	39	54.9	298	7	AD2346	othetical pr
	39		531	7	~#	-
	39	54.9	558	~	T17324	
15	38		223	0	T37974	probable peroxisom
16	38		238	ď	T40568	hypothetical profe
17	38		275	2	T22597	hypothetical prote
18	38	53.5	323	N	C82234	, 5
79	38		335	N	T33211	hypothetical prote
20	38		393	7	D71876	
21	38	53.5	515	~	51	probable cytochrom
22	38		543	7	T00513	cytochrome P450 ho
23	38	53.5	932	7	T28820	al pro
24	38		1436	~	F86904	μ
25	37		9	~	C97838	hypothetical prote
56	37.		283	~	7237	ra
27	37	52.1	7	7	6708	
28	37	52.1	Ø.	(1	9	0
29	37	52.1	464	7	AI2343	

hypothetical sh3-c	probable cytochrom	diphosphate-fructo	hypothetical prote	outer capsid prote	resistance protein	cell division prot	probable C-factor	ornithine decarbox	probable protein k	T14P4.7 protein -	CPE-binding protei	hypothetical prote	hypothetical profe	lactotransferrin	hypothetical prote
T39801	B84514	T01470	T19429	A45687	T30563	H64185	C82155	\$52784	B96547	E86156	A55377	E64464	T34079	TFBOL	T25415
11 2	18 2	33 2	31 2	19 2	2	5 2	5 2	5 2	16 2	3	1	7	2	1	2
5(518	25	99	74	180	4.2	23	43	476	51	56	9	99	70	74
52.1	52.1	52.1	52.1	52.1	52.1	51.4	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7	50.7
37	37	37	37	37	37	36.5	36	36	36	36	36	36	36	36	36
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

RESULT 1

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C.Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C.Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000; S74.
actotransferrin precursor [validated] - human
                                                                                                                                                                                                                                            submitted to the EMBL Data Library, March 1994 A;Reference number: G06820 A;Accession: G01394
                                   N;Alternate names: lactoferrin
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence r
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A; Status: preliminary; translated from GB/EMBL/DDBJ

A,Molecule type: mRNA A,Residues: 1-711 <CHO> A,CTOSB-references: EMBL:007643; NID:9467236; PIDN:AAB60324.1; PID:9467237 B,Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucleic Acids Res. 18, 5288, 1990 A;Title: Complete nucleotide sequence of human mammary gland lactoferrin. A;Reference number: S11228; MUID:90384839; PMID:2402455

A; Accession: S11228

A; Molecule type: mRNA
A; Residues: 1-148, T., 150-422, C', 424-711 < REY>
A; Residues: 1-148, T., 150-422, C', 424-711 < REY>
A; Cross-references: EMML:X53961; NID:334415; PIDN:CAA37914.1; PID:934416
A; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A; Title: Differential molecular mechanism of the estrogen action that regulates lactofer: A; Reference number: A45401; MUID:93125571; PMID:1480183

A; Accession: A45401

A; Molecule type: DNA
A; Residues: 1-15 < TEN>
A; Cross-references: GB-52659; NID:g263311; PIDN:AAB24877.1; PID:g263312
A; Experimental source: placenta
A; Note: sequence extracted from NCBI backbone (NCBIP:122202)
A; Powell, M.J; Ogden, J.E.
Nucleic Acids Res: 18, 4013, 1990
A; Title: Nucleotide sequence of human lactoferrin cDNA.
A; Reference number: S10324; MUID:90326549; PMID:2374734

A; Accession: S10324

A; Molecule type: mRNA A; Residues: 3-711 <POW>

A,Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R,Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Bjochem. J. 276; J49-355, 1991
A;Tille: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066

A, Status: nucleic acid sequence not shown; not compared with conceptual translation A; Accession: S15853

A; Molecule type: mRNA A; Residues: 20-31 <ST1>

A;Accession: \$20841 A;Molecule type: protein A;Residues: 20-28,'X',30-31 <ST2>

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Gaps

· 0

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lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Species: 14-Unl-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
B;Otan, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biophys. Acta 1243, 25-32 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet a A;Reference number: S52107; WUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Firstkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, H. T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authorer: Parry, C.; Quali, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serox A;Reference number: ABD502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NiAlternate names: lactotransferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                  Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      67.6%; Score 48; DB 2; Length 33; 54.5%; Pred. No. 0.07;
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                                                                                                                       1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-33 «QIA»
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 42; DB 2; 58.3%; Pred. No. 13;
                                                  Score 51; DB Pred. No. 0.443; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Mismatches
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                                               71.8%;
          Query Match
Best Local Similarity 63.0
To Conservative
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                                                                                                                                                                                                                                                         38 CYOWORRMRKL 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
Matches 6; Conserv
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Matches 7; Conserv
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A; Status: preliminary
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A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A;Note: this is the final paper in a series
R;Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
Bur. J. Biochem. 241, 303-308, 1996
A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A;Reference number: S74119; MUID:97054624; PMID:8898921
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                                                                                                                                                                                                                                                                                                                                            A, Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 3-701, 'SWKPVN' <PAN>
A; Residues: 3-701, 'SWKPVN' <PAN>
A; Residues: 3-701, 'SWKPVN' <PAN>
A; Macurian to normal breast tissue
R; Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Bur. J. Biochem. 145, 659-666, 1984
A; Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A; Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;360-699/Domain: transferrin repeat homology <PRH2>
F;29-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rile Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Blochem. Blophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A;Reference number: GC2323; MUID:94380047; PMID:89033048
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C;Keywords: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding mite: carbohydrate (Amn) (covalent) #status predicted
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression
A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Recession: S07160
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                                          A;Residues: 436-487,'A',489-711 cRAD>
A;Cross-references: EMBL:M18642; NID:g186815; PIDN:AAA86665.1; PID:g386855
R;Panella, T.J.; Liu, Y.; Hang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
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C; Superfamily: transferrin, transferrin repeat homology
C; Superfamily: transferrin; transferrin binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRHI>
                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A61169; MUID:91235214; PMID:1674448
A; Accession: A61169
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: GDB:119368; OMIM:150210
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Matches 11; Conservative
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A; Residues: 1-708 <LEP>
                                                                                                                                                                             A; Molecule type: mRNA
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Query Match

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A; Accession: A28438

A; Accession: A41205

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A;Map position: IX
A;Introns: 4862; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 1
3334/3; 3686/3; 3882/3; 4240/3
C;Superfamily: dynein heavy, chain, ciliary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 113, 283-284, 1992
A;Title: Cloning of a CDNA encoding the ovine interleukin-2 receptor 55-kDa protein, CD2£
A;Reference number: JC1113; MUID:92241682; PMID:1572550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK ce C; Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology C; Keywords: cytokine receptor; duplication; glycoprotein; T-cell proliferation; transmemb E; 1-21/Domain: signal sequence #status predicted <SIG> F; 22-275/Product: interleukin-2 receptor alpha chain #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, December 1991
A,Description: Molecular cloning, expression and characterisation of the ovine IL-2R alph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: mRNA
A;Residues: 1-165,'S',167-275 <VER>
A;Cross-references: EMBL:Z11560; NID:g1275; PIDN:CAA77652.1; PID:g1276
C;Complex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains;
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C.Species: Ol-Sep-1998 #sequence revision 11-Sep-1998 #text_change 22-Jun-1999
C.Accession: JC1133, S18899; S18910
G.Accession: JC1133, S18899; S18910
Gene 113, 283-284, 1992
                                                A,Molecule type: DNA
A,Residues: 1-4568 «MIT>
A,Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
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F;24-77/Domain: complement factor H repeat homology <FH1>
F;123-184/Domain: complement factor H repeat homology <FH2>
F;244-264/Domain: transmembrane #status predicted <TMM>
F;265-275/Domain: intracellular #status predicted <INT>
F;24-64,51-77,123-168,152-184/Disulfide bonds: #status predicted
F;80/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       57.7%; Score 41; DB 2; Length 4568; 41.7%; Pred. No. 1.7e+02; Live 4; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                   C;Keywords: nuclectide binding; P-loop
F;1913-1926(Region: nucleotide-binding motif A (P-loop)
F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
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                  A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                             A; Experimental source: strain 21gr
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A; Residues: 1-275 <BUJ>
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C;Accession: A28438; A41205
V;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
A;Reference number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein MYPU_5500 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C.Species: Mycoplasma pulmonis
C.Species: Mycoplasma 02-4-May-2001 #sequence of the murine respiratory pathogen Mycoplasma pulm
A.Reference number: A99512; MUID:21267165; PMID:11353084
A.Accession: F90580
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J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: 216302; MUID:94274778; PMID:8006077
A;Accession: T08030
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A;Cross-references: GB:AL445566; PID:g14089965; PIDN:CAC13723.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
                                                                                                                                                                                                          A.Molecule type: mRNA
A.Residues: 3-707 <PEN>
A.Cross-references: EMBL:J03298
R.Liu, Y., Teng, C., 21880-21885, 1991
A.Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A.Reference number: A41205; MUID:92042099; PMID:1939212
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C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 17;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: DNA
A;Residues: 1-15 <LIU>
A;Cresidues: 1-15 <LIU>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dynein beta heavy chain - Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
```

6; Conservative

Matches

Local Similarity

Query Match

A, Genetic code: SGC3

A; Gene: MYPU 5500

Genetics:

A; Molecule type: DNA

20 FAWONNIKKI 29

C; Accession: T08030

2 FQWQRNMKKV 11

à

54.5%;

Query Match
Best Local Similarity 54.57
Matches 6; Conservative

g

Tue Dec

A; Accession: S07442

```
A)Notes Nostocs op. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120 (5)Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 (5,Date: 14-Dec-2001) #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002 (5,Rocession: AD2346 ) A: Note, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res: 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana A;Reference number: AB1807; WUID:21595285; PMID:11759840
                            C;Species: nucleomorph Guillardia there in the control of a cukaryotic endosymbiont binote: nucleomorph is the vestigial nucleus of a cukaryotic endosymbiont c;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001 C;Accession: E90094

R;Douglas, S; Zauner, S; Fraunholz, M; Beaton, M; Penny, S; Deng, L.T.; Wu, X.; Rei Mature 410, 1091-1096, 2001

A;Title: The highly reduced genome of an enslayed algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bn/Spm-like transposon protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84471
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 402, 761-768, 1999
Affilte: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: A84471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AF165818; NID:g13794510; PIDN:AAK39885.1; GSPDB:GN00150
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 39; DB 2; Length 205;
Pred. No. 17;
3; Mismatches 3; Indels
26S proteasome SU B5 [imported] - Guillardia theta nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-205 < DOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Genome: nucleomorph
C; Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 FOWORNMKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                 A; Accession: E90094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: prsB5
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Matches
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C;Species: Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84325
R;NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
F,NG, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S
Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li
A;Title: Genome sequence of Halobacterium species NCC-1.
                                                             interleukin-2 receptor alpha chain precursor - bovine
NyAlternate names: CD25
NyAlternate names: CD25
C;Species: Bos primigentus taurus (cattle)
C;Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 22-Jun-1999
C;Accession: S07442
R;Weinbersy, A.D.; Shaw, V.; Paetkau, V.; Bleackley, R.C.; Magnuson, N.S.; Reeves, R.; Ma |
Immunology 63, 603-610, 1988
A;Title: Cloning of CDNA for the bovine IL-2 receptor (bovine Tac antigen).
A;Reference number: S07442; MUID:88212503; PMID:2835311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A penciption: receptor for interleukin-2
A Pathway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK c
A; Pathway: interleukin-2 receptor alpha chain; complement factor H repeat homology
C; Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology
C; Keywords: cytokine receptor; duplication; glycoprotein; T-cell proliferation; transment
F; 1-21/Domain: signal sequence #status predicted <SIG>
F; 2-275/Product: interleukin-2 receptor alpha chain #status predicted <MAT>
F; 2-43/Domain: extracellular #status predicted <ERT>
F; 24-77/Domain: complement factor H repeat homology <FH2>
F; 24-64/Domain: transmembrane #status predicted <IMT>
F; 24-64/Domain: intracellular #status predicted <IMT>
F; 24-57/Domain: intracellular #status predicted <IMT>
F; 24-64, 51-77, 123-168, 152-184/Disulfide bonds: #status predicted
F; 80, 109/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-275 <WEI>
A;Cross-references: EMBL:M20818; NID:g163208; PIDN:AAA51414.1; PID:g163209
C;Complex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
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0
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0

Score 40; DB 1; Length 275;

Pred. No. 15; 0; Mismatches

56.3%;

Query Match Best Local Similarity 58.3-7; Conservative

261 CLIWORKWKKNR 272

1 CFOWORNMKKVR 12

à

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|| |:::|:: |
445 CFTWRKDMERKR 456
1 CFQWQRNMKKVR 12
à
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56.3%; Score 40; DB 2; Length 584; 41.7%; Pred. No. 32;

2; Indels

5; Mismatches

Conservative

Best Local Similarity

Matches

A;Gene: VNG1732C Query Match

A, Status: preliminary A, Molecule type: DNA

A;Accession: C84325

RESULT 11

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A;Accession: T37974
A;Scatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Acidecule type: DNA
A;Residues: 1-223 <MUR>
A;Residues: 1-223 <MUR>
A;Residues: BMBL:Z69909; PIDN:CAA93785.1; GSPDB:GN00066; SPDB:SPAC19G10.03c
A;Experimental source: strain 972h-; cosmid c19G10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable peroxisomal membrane protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 28-Jul-2000
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                                                                A; Cross-references: GB: AE002093; NID: 94586022; PIDN: AAD25641.1; GSPDB: GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T17324
R;Duesterhoeft, A.; Lauber, J.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
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A;Introns: 10/3; 170/2
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPBC582.09
C;Keywords: peroxisome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T37974

R; Murphy, L; Harris, D; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, March 1996
A; Reference number: Z21759
                                                                                                                                                                                                                                                      0;
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0
                                                                                                                                                                                             54.9%; Score 39; DB 2; Length 531; 87.5%; Pred. No. 44; 1; Indels tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     53.5%; Score 38; DB 2; Length 223; 41.7%; Pred. No. 28; ive 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.9%; Score 39; DB 2; Length 558;
54.5%; Pred. No. 46;
tive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Accession: T17324
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-558 < DUE>
A;Cross-references: EMBL:AL117610
A;Experimental source: fetal brain; clone DKPZp564P2063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein DKFZp564P2063.1 - human (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 41.77
Thea 5; Conservative
                                                                                                                                                                                          Query Match
Best Local Similarity 87.5
Matches 7; Conservative
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Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: SPDB:SPAC19G10.03c
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                    A; Molecule type: DNA
A; Residues: 1-531 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Note: DKFZp564P2063.1
                                                                                                                                                                                                                                                                                                                                              501 OWFRINKK 508
                                                                                                                                                                                                                                                                                               3 QWQRNMKK 10
A;Status: preliminary
                                                                                             C;Genetics:
A;Gene: At2g05650
A;Map position: 2
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Search completed: February 21, 2003, 07:47:55 Job time : 10.65 secs
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec

US-09-743-107B-83

1 CFQWQRNMKKVR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P02788 homo sapien	n0 camel	capra h					_	Q10333 schizosacch		Q9vnb3 drosophila	9	P45068 haemophilus	4	8 drosophil		P49725 panagrellus	Q11100 caenorhabdi	_	Q15398 homo sapien	~	sorgh		P41187 liberibacte		_	_		_	٠.		6929	7163
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PDI1 HUMAN	DBF4_YEAST	KDG1_ARATH	BP28 DROME	COA2 HUMAN	RL28_BACST	RL28_LISMO	RL28 STAAM	RL28 THETN	SYB2_RHIME	YE83 METUA	Y495_SYNY3
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49.3	49.3	49.3	49.3	49.3	47.9	47.9	47.9	47.9	47.9	47.9	47.9
35	35	35	35	32	34	34	34	34	34	34	34

ALIGNMENTS

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PDB;
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Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                                                                                                                                   "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of
                                                                                                                                                                                                                                                                                                                 Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-82262043; PubMed-7049727;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedle J.W.,
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                                                                                                                          SEQUENCE OF 20-711.

MEDLINE=85076667; PubMed=6510420;
Metz-Boutique M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
Eur. J. Blochem. 145:659-666 (1984).
                                                                                                                                                                                                                                                                              PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
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Haridas M., Anderson B.F., Baker B.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sagripanti J.L.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An 88 amino acid long C-terminal sequence of human
                                                      Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA."; Nucleic Acids Res. 18:4013-4013(1990).
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                                                                                                                                                                                                                                                                                                                                                                                          N- and C-terminal domains.";
Biochim. Biophys. Acta 670:243-254 (1981).
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MEDLINE=99190892; PubMed=10089347;
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                   TISSUE=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
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MEDLINE=88001031; PubMed=3477300;
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 SEQUENCE OF 3-711 FROM N.A.
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Mintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,

A Qumsiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,

Sugar J., Kumaramanickavel G., Munier F., Schorderer D.F.,

B. Matri L., Iwata F., Kalser-Kupfer M., Nagata M., Nakayasu K.,

B. Hejtmancik J.F., Teng C.T.;

"Familial aubepithelial orneal amyloidosis (gelatinous drop-like
"Corneal dystrophy): exclusion of linkage to lactoferrin gene.";

Mol. Vision 4:31-32(1998).

C. - FONGTION: TRANSFRERING ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

C. - FUNCTION: LACTOFERROXINS A, B AND C HANE OPIOID ANTAGONIST

ACTIVITY: LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE

LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE

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                                                                                                                                                                                                                                                                                                         CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                            Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker E.N.; "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Agric. Biol. Chem. 54:1803-1810(1990).
                                                                              Acta Crystallogr. D 55:403-407(1999).
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EMBL; M93150; AAA36159.1;
EMBL; M83202; AAA58511.1;
EMBL; M83205; AAA58656.1;
EMBL; M18642; AAA86665.1;
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PubMed=9873069;
                                                                                                                                                                                                                                                                                                                                                                                                                  from human lactoferrin.
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1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
1LFH; 31-OCT-93.
1LFI; 31-OCT-93.
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1VFD;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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TISSUE-Mammary gland;

Paramasivam M., Stinivasan A., Singh R., Sahani M.S., Singh T.D.;

Paramasivam M., Stinivasan A., Singh R., Sahani M.S., Singh T.D.;

Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

-! FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE BY SIMILARITY).

-! SUBJUNT: MONOMER (BY SIMILARITY).

-! SUBJUNT: MONOMER (BY SIMILARITY).

-! SUBJUNT: COMPOSED OF TWO HOMOLOGUS DOMAINS.

-! SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                          Gaps
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Mammalia, Eutheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IRR01156; Transferrin.
Print; Pro0405; Lransferrin; 2.
PRINTS; PRO0402; TRANSFRRIN.
SWART; SM00094; TR FRR; 2.
PROSTIE; PS00205; TRANSFERRIN, 1; 2.
PROSTIE; PS00206; TRANSFERRIN, 2; 2.
PROSTIE; PS00207; TRANSFERRIN, 2; 2.
PROSTIE; PS00207; TRANSFERRIN, 3; 2.
Iransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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95.8%; Score 68; DB 1; Length 711; 91.7%; Pred. No. 0.00022;
                                                       0; Indels
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16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN
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                                                       11; Conservative
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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BY SIMILARITY.
IRON 1 (BY SIMILARITY).
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IRON 2 (BY SIMILARITY).
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TISSUBE Ammmary gland;
Liee T., Yu. D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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708 AA;
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Best Local Similarity
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TRFL CAPHI
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TRFL HORSE 077811;
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                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                          HSSP; 077698; 1CE2.
InterPro; IRR001156; Transferrin.
Pfam; PF00402; transferrin. 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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ANION (BY SIMILARITY)
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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L -> R (IN REF. 2).

Q -> K (IN REF. 2).

F -> R (IN REF. 2).

S -> R (IN REF. 2).

D -> G (IN REF. 2).
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EMBL; X78902; CAASS517.1; -.
HSSP; O77698; 1CE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resolution.";
J. Mol. Biol. 289:303-317(1999).

-1. FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
-1. FUNCTION: TRANSFERRINS ERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AJ010930; CAA09407.1; -.

R DDB; 1B1X; 02-DEC-98.

R DDB; 1B7Z; 02-EEB-99.

R PDB; 1B7Z; 02-FEB-99.

R InterPro; IPR001156; Transferrin.

R PRINTS; PR00425; TRANSFERRIN.

R PRINTS; SM00094; TR FER; 2.

R PROSTITE; PS00205; TRANSFERRIN 1; 2.

R PROSTITE; PS00206; TRANSFERRIN 2; 2.

R PROSTITE; PS00207; TRANSFERRIN 2; 2.

R Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Iron Transport; Glycoprotein; Metal-binding; Glycoprotein; Glycoprotein; Metal-binding; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                         Būkaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Perissodactyla; Equidae; Equus.
                                                                                                                                                                                                                                                                                                                                     Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.; "CDNA sequence of mare lactoferrin."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                       15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SUBCELLULAR LOCATION: Secreted.
-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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695 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
                                            15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last seq.
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                             NCBI_TaxID=9796;
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MEDLINE=92042099; PubMed=1939212;
Liu Y., Teng C.T.;
"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991)
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION. USUALLY BICARBONATE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                              (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
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Pred. No. 0.44;
2; Mismatches 1; Indels
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                     07BB84D50E1B165D CRC64;
                                                                                                                      IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
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-1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P08071; P70690; Q61799; Q922P2; (1707) P01-AUG-1988 (Rel. 08, Created) P15-UUN-2002 (Rel. 41, Last sequence update) P15-UUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Uterus;
MEDLINE=87280033; Pubmed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                        75991 MW;
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Similarity 75.0%;
9; Conservative 2
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                                                                                                                                                                                                                                                                                                                                                                             482
695 AA;
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N-LINKED (GLCNAC. .) (POTENTIAL).
MR -> 10G (IN REF. 1).
MR -> 0 (IN REF. 2).
MR -> 1 (IN REF. 2).
S -> T (IN REF. 2).
S -> T (IN REF. 2).
L -> 0 (IN REF. 1).
E -> G (IN REF. 1).
E -> G (IN REF. 1).
MY, F26AE0340A4C19AB CRC64;
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                                                                                                                                                                                                                                                       PROSITE; PS00205; TRANSFERIN 1; 1.
PROSITE; PS00206; TRANSFERIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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BY SIMILARITY.
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
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LACTOTRANSFERRIN
                                                                                                            EMBL; J03298; AAA40525.1; --
EMBL; B08510; BAA13633.1; --
EMBL; BC006904; AAH06904.1; --
EMBL; M74778; AAA39427.1; --
FTR; A26438; A28438.
HSSP; P02788; 1CE6.
MGD; MGI:96837; Ltf.
InterPro; IPR001156; Transferrin.
Ffan, PF00405; Lransferrin, 2.
PRINTS; PR00422; TRANSFERRIN.
SWART; SM00094; TR_EER; 2.
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Best Local Similarity
6, Conserve
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707 AA;
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37 CLRWONEMRKV 47

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Eukaryota, Actazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea, Bovidae, Bovinae, Bos.
01-OCT-1989 (Rel. 12, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
11t-cleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
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  SOUR THE TEST TEST TO DESCRIPTION OF THE SECOND OF THE SEC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J. Cell Sci. 107:635-644 (1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=21gr;
MEDLINE=94274778; PubMed=8006077;
Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYNEIN HAS ATPASE ACTIVITY.
-!- SUBUNT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                     Chlamydomonas reinhardtii.
Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
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MICROTUBULE-BINDIAG (POTENTIAL).
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InterPro; IPR004273; Dynein_heavy.
Bram; PF05028; Dynein_heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.
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69;
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(POTENTIAL).
9A9A5393C7C36AE7 CRC64;
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                                                                                                                               01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
OPAH OR ODA-4 OR SUP1.
                                                                                          PRT; 4568 AA.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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J. Cell Sci.
                                                                                     DYHB CHLRE
Q39565;
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SEQUENCE
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                                            RESULT 6
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275 A.A.

PRT;

STANDARD;

IL2A BOVIN P12342;

IL2A_BOVIN

RESULT 7

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01-0CT-1989 (Rel. 12, Created)

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                                                                                                                                                                                                                   MEDLINE=96116968; PubMed=6863178;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Yoo 'J., de Leon F.A., Stone R.T., Beattie C.W.;

Mamm. Genome 6:751-753(1995)

-!- FONCTION: RECEPTOR FOR INTERLEUKIN-2.

-!- SUBUNIT: NON COYALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R

EXIST IN 3 DIFFERENT FORMS: A HIGH AFPINITY DIMER, AN INTERMEDIATE

AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE

WITH A GAMMA CHAIN.
SEQUENCE FROM N.A.
MEDLINE=88212503; PubMed=2835311;
Weinberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S.,
Reeves R., Magnuson J.A.;
"Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).";
Immunology 63:603-610(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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SIGNAL 1 21
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-!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
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BY SIMILARITY.
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0; Mismatches
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SUSHI 2.
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HSSP; P01589; 11LM.
InterPro; IPR000436; Sushi_SCR_CCP.
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                                                                                                                                                                                                 SEQUENCE OF 1-21 FROM N.A.
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nes 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
-1- SUBGNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
-1- SUBGNIT: NON CONALENT PORMS: A HIGH AFFINITY DIMER. AN INTERREDIATE
--- BEXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERREDIATE
--- AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
--- SUBCELLULAR LOCATION: Type I membrane protein.
--- SUBCELLULAR LOCATION: 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92241682; PubMed=1572550;
Bujdoso R., Sargan D.R., Williamson M.L., McConnell I.,
"Cloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa
                                                                                                                                                                                                        Ovis aries (Sheep).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                             01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-FBB-1996 (Rel. 33, Last amnotation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (PS5) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INTERLEUKIN-2 RECEPTOR ALPHA CHAIN.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor; Repeat; Signal; Sushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            56.3%; Score 40; DB 1; Length 275; 58.3%; Pred. No. 6.4; tive 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=T-cell;
Verhagen A.A.;
Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S -> T (IN REF. 2).
1101A2DE5AC5A088 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC.
     275 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z11560; CAA77652.1; -.
EMBL; A19167; CAA42723.1; -.
EMBL; A19167; CAA01447.1; -.
PIR, S18910; S18910.
PIR, S18999; S18899.
PIR, JC1113; JC1113.
HSSP; PO1589; IIIM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               166 S
30904 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transmembrane; Glycoprotein;
STANDARD;
                                                                                                                                                                                                                                                                                                Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gene 113:283-284 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00084; sushi; ;
SMART; SM00032; CCP; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          275
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Best Local Similarity
7; Conserve
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275 AA;
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                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD25."
L2A SHEEP
                                                                                                                                                                                                                                                                                                  Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM
DOMAIN
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                            P26898;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AL096788; CAB46672.1; -.
Hypothetical protein.
SEQUENCE 238 AA; 26479 MW; 58095AA8CD708180 CRC64;
                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                             01-OCT-1996 (Rel. 34, Created)
116-OCT-2001 (Rel. 40, Last sequence update)
116-UNN-2002 (Rel. 41, Last annotation update)
Hypothetical protein C582.09 in chromosome II.
                                                                            Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                              MEDLINE=21848401; PubMed=11859360;
          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Conservative
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                                                                                                            Schizosaccharomyces.
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Best Local Similarity
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                                                                                                                       NCBI_TaxID=4896;
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Conservative

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                                                                                                                                                                                                                                   Karthikeyan S., Paramasivam M., Yadav S., Srinivasan A., Singh T.P.; "Structure of buffalo lactoferrin at 2.5-A resolution using crystals grown at 303 K shows different orientations of the N and C lobes."; Acta Crystallogr. D 55:1805-1813(1999).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
                                                                                  Bubalus bubalis (Domestic water buffalo).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bubalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001156; Transferrin.
Pfam, PF00405; transferrin; 2.
PRINITS, PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                  SEQUENCE FROM N.A.
Paramasivam M., Thattaliyath B.D., Kumar A., Srinivasan A.,
Singh T.P.;
                                                                                                                                                                                "CDNA sequence of Buffalo lactoferrin.";
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                     -!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LACTOTRANSFERRIN
                              15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin),
           708 AA
                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRON 1.
                                                                                                                                                                                                                                                                                                                          !- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                            MEDLINE=20003130; PubMed=10531476;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ005203; CAA06441.1; -. PDB; 1CE2; 19-MAR-99.
           STANDARD;
                                                                                                                                                                                                                                                                                                                 -! - SUBUNIT: MONOMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Signal; 3D-structure.
                                                                                                                              NCBI_TaxID=89462;
         TRFL_BUBBU
077698;
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STRAINE-BETKELEY,

REDILINE-20196006; PubMed=10731132;

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,

Adams M.D., Celniker S.E., Hill P.W., Hoskins M.H., Galle R.F.,

George R.A., Lewis S.E., Richards S., Champen M., Pfeiffer B.D.,

Baradon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

An Endow R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

An Endow R.C., Rogers Y.H.C., Blazel R.G., Helt G., Nelson C.R., Miklos G.L.G.,

Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Baus M., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

Burkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

Burkova D., Botchan M.R., Douck J., Brokstein P., Brottier P.,

Burkova D., Botchan M.R., Dong Z., Mays A.D., Dew I., Dietz S.M.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

Burtis K.C., Bvangelista C.C., Ferrac Z., Ferriera S., Fleischmann W.,

An Horbin K.J., Bvangelista C.C., Ferrac S., Dunkov B.C., Dunn P.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Marvey D., Heiman T.J., Mei M.-H., Ibegwam C.,

Ander B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Ander B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Ander B.B., McIntosh T.C., McLeod M.P., Mochreson D.L.,

RA Merkulov G., Milshina N.V, Mobarry C., Morris J., Moshrein D.,

Rander S.M., Moy M., Murphy B., Murphy L., Murphy L., Pauley D., M., Resee M.G.,

Rander E.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

Shieb E.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,

Shieb E.C., Siden-Klamos I., Sunders R., Venter E., Wang A.H., Wang X.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perrygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophil;dae; Drosophila.
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IRON 1.
IRON 1.
IRON 2.
IRON 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08D2600AAB2F9ACD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 40, Created)
(Rel. 40, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77729 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.5%;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    708 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
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2412
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6144
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15-JUN-2002
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Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.; "Identification and baculovirus expression of the VP4 protein of the

MEDLINE=93233240; PubMed=8386274;

SEQUENCE FROM N.A.

human group B rotavirus ADRV.";
J. Vărol. 67.2730-2738(1993)
-!- SUBCELLULAR LOCATION: Outer capsid.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.

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Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Xe J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; science 287:2185-2195 [2000]
                                                                                                                                                   Unpublished observations (MAY-2001).
-!- FUNCTION: PROBABLE ROLE IN THE ODORANT RESPONSE, BEING AN ODORANT
                                                                                                                                                                                                                                            -!- CAUTION: Ref.1 sequence differs from that shown due to erroneous
                                                                                                                                                                                               SUBCELLULAR LOCATION: Integral membrane protein (Potential). SIMILARITY: BELONGS TO FAMILY DR-OR OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; Transmembrane; G-protein coupled receptor; Olfaction; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.1%; Score 37; DB 1; Length 453; 66.7%; Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 (FOIENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LINKED (GLCNAC. . .) (Po
4B660B3380901192 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOPLASMIC
                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE003603; AAF52033.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52272 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0037322; Or83a.
InterPro; IPR004117; 7tm_6.
                                                                                                                                                                                                                                                          gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02949; 7tm 6; 1.
Hypothetical protein; Tr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49
85
148
169
                                                                                                                        CONCEPTUAL TRANSLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      453 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29
50
86
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           360
381
409
430
249
                                                                                                                                      Robertson H.M.;
                                                                                                                                                                                                                               RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3lycoprotein;
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TRANSMEM
DOMAIN
TRANSMEM
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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0;

Gaps

.. 0

6; Indels

0; Mismatches

Conservative

. 9

Matches

1 CFQWQRNMKKVR 12

ઠે

Score 37; DB 1; Length 749; Pred. No. 58;

52.1%; 50.0%;

Query Match Best Local Similarity

D1223527DEAE0F21 CRC64;

84362 MW;

749 AA;

SEQUENCE

(POTENTIAL).

(POTENTIAL)

(GLCNAC. (GLCNAC

N-LINKED N-LINKED N-LINKED N-LINKED

InterPro; IPR000416; Cap_VP4. Pfam; PF00426; VP4; 1.

EMBL; M91434; AAA47338.1;

Glycoprotein.

Coat protein;

CARBOHYD CARBOHYD CARBOHYD (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).

(GLCNAC. (GLCNAC. (GLCNAC. .

N-LINKED N-LINKED N-LINKED

53 109 133 407 568

CARBOHYD

CARBOHYD CARBOHYD CARBOHYD CARBOHYD CARBOHYD

(GLCNAC. .

(GLCNAC (GLCNAC

N-LINKED N-LINKED N-LINKED

(POTENTIAL)

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"Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95350630; PubMed=7542800; Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness B.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutlon G., Fitzhugh W., Fields C.A., Gocayne J.D., Sott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Wieldman J.E., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
-!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN ANOMALOUS FILAMENT
GROWTH (BY SIMILARITY). MAY BE A COMPONENT OF THE SEPTUM. IT
                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
NCBI_TaxID=727;
                                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Cell division protein ftsA.
                                                                                                   STANDARD;
                                                                                                                                                                                                                                      Haemophilus influenzae.
195 CFTWDMNCANVR 206
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                   Cell division
FTSA OR HII142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter J.C.;
                                                                                                 FTSA HAEIN
P45068;
                                                                              FTSA HAEIN
d
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.. 0

Gaps

.. 0

1; Indels

2; Mismatches

Conservative

Matches

a

Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).

01-JUN-1994 (Rel. 29, Created) 01-JUN-1994 (Rel. 29, Last sequence update) 01-JUN-1994 (Rel. 29, Last annotation update)

749 AA.

PRT;

STANDARD;

VP4 ROTGA

VP4 ROTGA

004916;

Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus)

Viruses; dsRNA viruses; Reoviridae; Rotavirus. NCBI_TaxID=12705;

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30-MAY-2000 (Rel. 39, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FROM N.A.
                                                    Nebula protein.
NLA OR CG6072.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                    females.
                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use. by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Boublik Y., Kouassi K.N., Cavallaro C., Bergoin M.; "Complete nucleotide sequence and genome organization of an infectious clone of Diatraea saccharalis densovirus (DSDNV)."; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; ssDNA viruses; Parvoviridae; Densovirinae; Densovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51.4%; Score 36.5; DB 1; Length 425; 63.6%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMS; TIGRO1174; FtsA; 1.
Cell division; Cell shape; Complete proteome.
SEQUENCE 425 AA; 45836 MW; AFSC4B808D73CB9D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 AA; 31154 MW; AA9B1B03D7718C71 CRC64;
MAY INTERACT WITH FTSZ (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FTSA/MREB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 40;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Diatraea saccharalis densovirus (DsDNV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF036333; AAC18000.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1999 (Rel. 38, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.78;
85.78;
                                                                                                                                                                                                                                                                                                                          EMBL; U32794; AAC22797.1; -. TIGR; H11142; -.
                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003494; FtsA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nonstructural protein NS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF02491, FtsA;
TIGRFAMS; TIGR01174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 CHODWONNLKK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQ-WQRNMKK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=72003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WORNMEK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 WORNWKK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nonstructural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VNS2 DSDNV
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VNS2_DSDNV
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Matches

292 AA.

NLA DROME STANDARD; 09X \overline{Z} LB; Q9V391; 30-MAY-2000 (Rel. 39, Created)

RESULT 15 NLA DROME

g

Matches

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RA Adams W.D. Celniker S.E. 11 P.W., Forens C.A., Gocayne J.D.,
RA Adams W.D. Celniker S.E. 11 P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Burdon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeeiffer B.D.,
RA Adams M.D. C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Adams K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Adams M.D. Bacul A., An H.-J., Andrews-Feanachch C., Baldwin D.,
RA Beeson K.Y. Benco P.V., Barenan B.P., Bhandari D., Bolshakov S.,
Bortchan M.R., Boul L.B., Bhandari D., Bolshakov S.,
Rokova D., Detchan M.R., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Perraz C., Ferriac S., Multon B.,
R. Dodson K., Doug L.B., Downess M., Dayan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doug L.B., Downess M., Dayan-Rocha S., Dunkov B.C.,
RA Glock A., Gong F. Gorrell J.H., Gu Z., Gabart W.M., Glasser K.,
A Glock A., Gong F. Gorrell J.H., Gu Z., Genbart W.M., Glasser K.,
A Hostin D., Houston K.A., Hawland T.J., Werlandez S.R.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Islang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Islang Y., Lin X.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Mchherson D.,
Mchallian S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Ralazzolo M., Pittuman G.S., Pan S., Pollard J., Puri V., Reede M. G.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun R.,
Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith H.O.,
Raliams S.M., Woodser T., Wand S., All, Wang X.,
Walliams S.M., Woodser T., Wang X., Mang Z.-Y., Wassarman D.A., Walner S.C., Who J., Stang S., Rang S.,
Ralinger C., Stapleton M., Stupski M.P., Smith H.O.,
Raliams S.M., Woodser T., Wang S., Zhan W., Sang S., Shith H.O.,
Raliams S.M., Woodser J., Sanger S., Shang S.,
Ralinger S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                  Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

NCHI_TAXID=7227;
                                                                                                                                                                                                                            SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
-!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
                                                                                                                                                                                                                                                                                                                        Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0026629; nla.
SEQUENCE 292 Aa; 31423 MW; 64FlBBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF147700; AAD33987.1; -. EMBL; AE003712; AAF55285.1; -.
```

Query Match 50.7%; Score 36; DB 1; Length 292; Best Local Similarity 45.5%; Pred. No. 34; Matches 5; Conservative 4; Mismatches 2; Indels

0;

0; Gaps

OY 2 FOWDRIMMKKVR 12
| | | | : : : |
| Db 150 FOWLRSFRRIR 160

Search completed: February 21, 2003, 07:27:58 Job time : 5.6 secs

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Query Match
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Matches
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Q8yp77 anabaena sp
Q9daz8 mus musculu
Q91zd5 mus musculu
Q91z75 mus musculu
Q81z75 hemeroulu
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Q8r2a4 mus musculu
Q38115 bacteriopha
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09hpa3 halobacteri
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Q9ucy5 homo sapien
Q9tr80 ovis aries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         salmonella
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118.873 Million cell updates/sec
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                                                                                                                                                                                February 21, 2003, 07:25:55; Search time 20.8 Seconds
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GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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Q98Q19
Q8R2A4
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Q9DAZ8
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Gapop 10.0 , Gapext 0.5
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Q9UCY5
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sp_human:*
sp_invertebrate:*
sp_mammal:*
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sp_virus:*
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sp_bacteriap:*
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Maximum DB seq
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Q77855 The numer of 77855 The numer immun Q77856 Thuran immun Q94454 Thuran immun Q94401 Sesamum ind Q9540 Genorhabdi Q95404 Aslicobacte Q25185 arabidopsis Q22188 arabidopsis
                                                                      O9jjz5 mus musculu
O19153 caenorhabdi
O9cdi2 lactococcus
                                                                                            Q72904 human immun
Q8rmb8 cytophaga j
Q8tnf5 methanosarc
streptomyce
arabidopsis
                    Ogrgt4 fusobacteri
Ogn906 trypanosoma
                                                                                   Q92g16 rickettsia
Q9d4t5 mus musculu
                                                                                                             Q9wyq1 thermotoga
Q9j196 mus musculu
Q91zf3 mus musculu
                                                                                                        ralstonia s
         Q9nz17 homo sapien
    Q9sic0
                                                                                                        Q8xse2
                                                     061888
09ZKP4
022185
022188
09JUZ5
019153
09CDIZ
09ZGL6
Q9RJP2
Q9SIC0
Q9NZL7
                 Q9UFK6
Q8RGT4
Q9N906
                            Q77855
Q77856
Q8Q454
Q9XHP1
                                             Q93780
Q9KSU3
                                                                                            Q72904
Q8RMB8
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                                                                                                                    Q91ZF3
            CONVEY
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11
15
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558
589
2186
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122
122
248
270
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ALI GNMENTS

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Gaps
                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                         .,
0
                                                                                                                                                                                                                                                                                                                                                                 Length 711;
                                                                                                                                                                                                                                                                                                                                                             Score 63; DB 4; Length 711
Pred. No. 0.0033;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                        Straubberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; -.
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 A.A.
                                         Created)
PRT;
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21,
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nes 10; Conservative
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PRELIMINARY;
                                                            (TrEMBLrel. (TrEMBLrel.
                                       01-JUN-2002 (TrEMBLrel.
                                                                                                                     Homo sapiens (Human)
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE=PROSTATE;
                                                                                                      Lactotransferrin.
                                                            01-JUN-2002
01-JUN-2002
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us-09-743-107b-83.rspt

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Gaps

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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J., Churcher C., Wannyall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G., "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             098019;
01-0CT-2001 (TrEMBLrel. 18, Created)
01-0CT-2001 (TrEMBLrel. 21, Last annotation update)
101-UN-2002 (TrEMBLrel. 21, Last annotation update)
17NA pseudouridine synthase B (TRNA pseudouridine 55 synthase) (PSI55
8ynthase) (Pseudouridylate synthase) (Uracil hydrolyase)
NYPU_5500.
genes that are differentially expressed at rice young panicle."; 2bubrited (APR-1999) to the EMBL/GenBank/DDBJ databases.
-1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AF140486; AAD29699.1; -.
PITGEPPC: PR001128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PR00385; P450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                         59.2%; Score 42; DB 10; Length 105; 70.0%; Pred. No. 3.2; 2; Indels cive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59.2%; Score 42; DB 16; Length 511; 58.3%; Pred. No. 17; 5.1ve 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 413:848-852(2001).
EMBL, AL627276, CAD06049.1, -.
Hypothetical protein; Complete proteome.
SEQUENCE 511 AA, 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                             SEQUENCE 105 AA; 11912 MW; B0EEFCDD487E19F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                             PROSITE, PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Monooxygenase; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                             511 AA.
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01-MAR-2002 (TrEMBLrel. 20, L
Hypothetical protein STX3070.
STX3070.
                                                                                                                                                                                                                                                                                                                                                                        Q8Z462;
Q8Z462;
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                            Query Match
Best Local Similarity 70.uv
Para 7; Conservative
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Matches 7; Conservative
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                                                                                                                                                                                                                                                                                            61 CPOWERLGKK 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=601;
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Q98Q19
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   SHANARARES SHE
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                                                                             Sato I.; "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa (Rice).
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzee, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu J., Yang J.; "Suppression subtractive hybridization (SSH) identified candidate
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                      83.1%; Score 59; DB 4; Length 38; 90.9%; Pred. No. 0.00082; cive 1; Mismatches 0; Indels
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HSSP, O77698; ICE2.
InterPro: IPRO01156; Transferrin.
Pfam; PPRO0405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                         0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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54.5%; Pred. No. 0.074;
cive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                         33 AA
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                                                                                                          seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
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                                             SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
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                                                                                                                                                         InterPro; IPR001156; Transferrin.
                                                                                                                                                                          Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0
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                                                                                                                                                                                                                                                          10; Conservative
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Best Local Similarity
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                NCBI_TaxID=9606;
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Q9TR80
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               Bacteriophage rlt.
                                NCBI TaxID=43685;
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Q9HPA3
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                                                                         MEDLINE=21267165; PubMed=11353084;
Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
Blanchard A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
MOBI_TaxID=10090;
                                                                                                                     "The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis."; Nucleic Acids Res. 29:2145-2153(2001).
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        Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Vomeronasal receptor VIRE6.
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Last annotation update)
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MEDLINE=21676859; PubMed=11802169;
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Mypulist; MYPU 5500; -..
InterPro; IRR004510; TruB.
InterPro; IRR005501; TruB.N.
Pfam; PR01509; TruB N; 1.
TIGRFAMS; TIGR00431; TruB; 1.
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EMBL; AY065506; AAL47911.1; -.
                  Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vlr vomeronasal receptors.";
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                                                                                                                                                                                                                         Lyase; Complete proteome.
                                                                                                                                                                                                                                                                                6; Conservative
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Mycoplasma pulmonis.
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Matches 6; Conserv
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                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  2 FOWORNMKKV 11
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Q38115;
01-NOV-1996 (
01-NOV-1996 (
01-NOV-1998 (
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MEDIINE=96332668; PubMed=8730874; MEDIINE=96332668; PubMed=8730874; Matuta A., Van Sinderen D., Karsens H., Smit E., Venema G., Kok J.; Inducible gene expression mediated by a repressor-operator system isolated from Lactococcus lactis bacteriophage rit."; Mol. Microbiol. 19:1331-1341(1996).
                                                                                                                                                                                                                                                                                                                   Venema G., Nauta A.;
"Sequence analysis and molecular characterization of the temperate "Sequence analysis and molecular characterization of the temperate actocococal bacteriophage rlt.";
Mol. Microbiol. 19:1343-1355 (1996).
EMBL, U38906; AAB18704.1; -.
SEQUENCE 469 AA; 53160 MW; 1F8E02D4325CGBB9 CRC64;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Steridae; euasterids II; Asterales; Asteraceae; Asteroideae;
Astereae; Callistephus.
NCBI_TaxID=13379;
                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE-96332669; PubMed-8730875;
Van Sinderen D., Karsens H., Kok J., Terpstra P., Ruiters M.H.,
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MATTERS S., FOrkmann G.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; API88612; AAF04115.1;
REMBL; API80612; AAF04115.1;
REMBL; APROMOS CYTOCHROME P450.
RPAINTS; PRO0385; P450.
RPROSITE; PRO0385; P450.
RPROSITE; PRO0386; CYTOCHROME P450; UNKNOWN_1.
RHOME, MONCOXYGENBASE; OXIGOREGICHESE.
SEQUENCE 514 AA; 58412 MW; 90B631B28952A5E7 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Matches 5; Conservative
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nes 6; Conservative
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NCBI_TaxID=10090;
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01-MAR-2002
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                                                                                                                                                                                                               MEDLINE=20504483; PubMed=11016950; Merquist B., Pan M., MEDLINE=20504483; PubMed=11016950; MG W.V., Kennedy S.P., Mahairas G.G., Thorseon V., Sbrogna J., Shukla H.D., Lasky S.R., Baliga N.S., Thorseon V., Sbrogna J., Swartzell S., Weir D., Hall T.A., Welti R., Goo Y.A., Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W., Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H., Isenbarger T.A., Per R.F., Pohlschroder M., Spudich J.L., Jung K.-H., Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D., Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.; "Genome sequence of Halobacterium species NRC-1."; Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
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MEDLINE=21223349; PubMed=11323671;
Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T., Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an enslaved algal nucleus.";
Nature 410:1091-1096(2001).
EMBL; AF165818; AAK39885.1; -.
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                                                                                  Halobacterium sp. (etrain NRC-1).
Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
Halobacteriaceae; Halobacterium.
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NCBI_TaxID=55529;
01-MAR-2001 (TrEMBLrel. 16, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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01-0CT-2001 (TrEMBLrel. 18, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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Interpro, IPR001353; Protsme_protease.
Pfam; PF00227; proteasome; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Interpro, IPR001646; Speptide repeat.
InterPro; IPR001622; K+channel pore.
Pfam; PF00805; Pentapeptide; 2.
Complete proteome.
SEQUENCE 584 AA; 65151 MW; 21BF5DF
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Best Local Similarity
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Les 5; Conserv
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                         NCBI TaxID=64091;
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RA Arakwa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., Rakwa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Yanada M., Nishi Y., Kiyosawa H., Kondo S., Yamanaka I., Radota Y., Okazaki Y., Gojbori T., Bono H., Kasukawa T., Saito R., Richi P., Isaito T., Sasto T., Radota K., Matsuda H., Rabburner M., Batalov S., Casavant T., Radota K., Matsudo Y., Kikaido I., Pesole G., Quackenbush J., Schrim L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Bakai K., Okido T., Furnon M., Anno H., Baldarelli R., Barsh G., Bakai K., Doffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.R., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sanaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Shashila S., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Harashizari Y., Harashizari Y., Romatizari Y., Kohtsuki S., Harashizari Y., Rawai Y., Kawaji H., Kohtsuki S., Harashizari Y., Hasegawa Y., Kawaji H., Kohtsuki S., Harashizari Y., Harashizari Y., Kawaji H., Kohtsuki S., Harashizari Y., Kawaji H., Kahashizari Y., Kawaji H., Kohtsuki S., Harashizari Y., Kawaji H., Kahashizari Y., Kawaji 
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MEDLINE=21595285; PubMed=11759840;
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Watanabe A., Irigudah M., Ishikawa A., Kawashima K., Kimura T.,
Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M.,
Yasuda M., Tabata S.,
"Complete genomic sequence of the filamentous nitrogen-fixing
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NCBL_TaxID=103690;
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DNA Res. 8:205-213(2001).
EMBL; AP003596; BAB76022.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 298 AA; 34513 MW; 64036E6B52299A9F CRC64;
                                                                                                                                                        (TrEMBLrel. 20, Created)
(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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MEDLINE=21085660; PubMed=11217851;
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01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2002 (TrEMBLrel. 20,
        PRELIMINARY;
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Nature 409:685-690(2001)

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STRAIN=C57BL/6J; TISSUE=PLACENTA; Deussing J., Schwinde A., Peters C.; Deussing J., Kouadio M., Rehman S., Werber I., Schwinde A., Peters C.; "Identification and Characterization of a Dense Cluster of Placenta-specific Cysteine Peptidases and Related Genes on Mouse Chromosome
                                                                                                                                                                                                               Gaps
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                  Score 39; DB 11; Length 332;
Pred. No. 38;
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                                                                                                                                                                                                               1; Indels
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EMBL; AY034574; AAKS8450.1; --
MGD; MGI:2151929; Cts3.
                                    MEROPS, COI.053, -..
MGD; MGI:1916256; 160000123R1K.
MGD; MGI:1916256; 160000123R1K.
InterPro; IPR000068; Peptidase_CI.
InterPro; IPR0000169; SHprot_assite.
PRINTS; PR007015; PAPAIN.
PRODINS; PR0001058; Peptidase_CI; 1.
PROSITE; PS00639; THIOL PROTEASE HIS; UNKNOWN 1.
SEQUENCE 332 AA; 37298 MW; 0804F1BA5E6538E0 CRC64;
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CATHEPSIN-3.
; 4184890725B41C0D CRC64;
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 21, Last annotation update)
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Last annotation update)
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InterPro; IPROGOGES, SHprot_acsite.
Pfam; PF00112; Peptidase_C1; 1.
ProDom; PD001158; Peptidase_C1; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
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55.6%; Pred. No. 30,
3; Mismatches
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             EMBL; AK005389; BAB23995.1; -. HSSP; P07711; 1CJL.
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114 332 C.
332 AA; 37326 MW;
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01-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-MAR-2002 (TrEMBLrel. 20, L
Cathepsin M.
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Best Local Similarity
Matches 5; Conserv
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Matches 5; Conserv
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01-DEC-2001
01-JUN-2002
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SIGNAL
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Q91275
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Q91ZD5
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 Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                   SEQUENCE FROM N.A.

STRAIN=129/SUFUTACFER; TISSUE=SPLEEN;
Rehman S., Peters C., Deussing J.;
Submitted (SEP-201) to the EMBL/GenBank/DDBJ databases.
Rehmin: AV057446; AA115416.1;
RIMEL; AV057446; AA115416.1;
RIMELPRO; IPRO0169; SEPTOT acsite.
Rem: PRO012; PRO0169; SHDTOT acsite.
Rem: PRO012; Peptidase Cl; 1.
Redon; PD000158; Peptidase Cl; 1.
Redout S. AR065178; PROTEASE HIS; UNKNOWN 1.
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                                                                                                                                                                                                                                                                                                                                                     1; Indels
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nes 5, Conservative
musculus (Mouse).
                                                     NCBI_TaxID=10090;
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52 WEENMKKIK 60
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GenCore version 5.1.3
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7 21, 2003, 07:25:55 ; Search time 28.3 Seconds	(without alignments) 56.502 Million cell updates/sec
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February 21,	
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US-09-743-107B-84 71 1 CFQWERNMRKVR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

A Geneseq 101002:* SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 SIDS2/gcgdata/geneseq/geneseqp-emb1/AA19 SIDS2/gcgdata/geneseqf/geneseqp-emb1/AA19 SIDS2/gc	_
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human lactoferrin									
SUMMARIES			ជា	~		AAY78046	AAY78047	AAY78037	AAY78048	AAY78049	AAY78036	AAY78050	AAY78051
			DB	21	21	21	21	21	21	21	21	21	21
		Query	Length	12	12	12	12	13	13	13	14	14	14
	مد	Query	Match	100.0	95.8	92.8	95.8	95.8	95.8	95.8	95.8	95.8	95.8
			Score	71	68	68	68	68	68	68	68	68	68
		Result	No.	1	7	3	4	S	9	7	80	σ	10

ALIGNMENTS

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AAY78084 standard; Peptide; 12 AA.
                                                                                                      25-APR-2000 (first entry)
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Human lactoferrin derived peptide SEQ ID NO:84.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

99WO-SE01230. WO200001730-A1. Homo sapiens. Synthetic. 06-JUL-1999; 13-JAN-2000.

98SE-0002562. 98SE-0004614. 98SE-0002441, (ASCI-) A+ SCI INVEST AB. 06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                     AAY78001 to AAY78100 represent peptides having sequences based on human
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colltis; Candida infection; fungicidal;
                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                   Claim 22; Page 36; 102pp; English
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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98SE-0002562.
98SE-0004614.
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Pred. No. 4.3e-05;
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                                                                                                                                                                                                                                                             AAY78047 standard; Peptide; 12 AA.
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                                                                                                                         95.8%;
91.7%;
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98SE-0002562.
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17-JUL-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections and a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an infant formula food. The peptides are also in food though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower cannot be used for the same purposes as lactoferrin at lower
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                                                                                                                                       AAY78037 standard; Peptide; 13 AA
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1 CFOWERNMRKVR 12
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17-JUL-1998;
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported binding to specific lactoferrin receptors and are then transported through the direculation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal in food stuffs such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tunoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower

AAY78001 to AAY78100 represent peptides having sequences based on human

Human lactoferrin derived peptide SEQ ID NO:49.

(first entry)

25-APR-2000

AAY78049

AAY78049 standard; Peptide; 13 AA.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through linding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                            Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection; fungicidal, bactericidal, preservative.
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Best Local Similarity
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intestine through the opecific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or trumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as an also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
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                                                                                                                           Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 21; Length 13;
Pred. No. 4.7e-05;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:36.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                      99WO-SE01230
                                                                                                                                                                                bactericidal; preservative.
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Best Local Similarity 91...
--- 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       (ASCI-) A+ SCI INVEST AB.
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                                                                                                                                                                                                                                                                   WO200001730-A1
                                                                                                                                                                                                                   Homo sabiens.
                                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                                                                                                                                      06-JUL-1999;
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                                                                                                                                                                                                                                                                                                    13-JAN-2000
                                                                                                                                                                                                                                     Synthetic.
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RXHXKX
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Gaps

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11; Conservative

Matches

1 CFOWERNMRKVR 12

2 CPOWORNMRKVR 13

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8

RESULT 7

98SE-0002441. 98SE-0002562. 98SE-0004614.

17-JUL-1998; 29-DEC-1998; 06-JUL-1998;

(ASCI-) A+ SCI INVEST AB.

99WO-SE01230

06-JUL-1999;

13-JAN-2000

WO200001730-A1

Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammatcions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also tingicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would contain at lower cannot be used for the same purposes as lactoferrin at lower
                 Human, lactoferrin, modification, infection, inflammation, tumour,
food, infant formula, anti-inflammatory, anti-microbial, anti-tumour,
urinary tract infection, colitis, Candida infection, fungicidal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                          98SE-0002562.
98SE-0004614.
                                                                                                                                                                                                                                         99WO-SE01230.
                                                                       bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB
                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-147388/13.
                                                                                                                                                               WO200001730-A1.
                                                                                                           sapiens.
                                                                                                                                                                                                                                     06-JUL-1999;
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                                                                                                                              Synthetic.
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Gaps .. 0 95.8%; Score 68; DB 21; Length 14; 91.7%; Pred. No. 5.1e-05; 1. Mismatches 0; Indels 11; Conservative Similarity 14 AA; Sequence Query Match Local Matches

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AAY78050 standard; Peptide; 14 AA. AAY78050; AAY78050

(first entry) 25-APR-2000

Human lactoferrin derived peptide SEQ ID NO:50.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

99WO-SE01230.

06-JUL-1999;

Homo sapiens

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tunnours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tunoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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                                                                                                                                                                                                                               Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                                                                                                                                          Hanson LA, Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bactericidal; preservative
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Matches 11; Conservative
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment to brough the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candia infection a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bacterrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower costs.
                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 68; DB 21; Length 14;
Pred. No. 5.1e-05;
1; Mismatches 0; Indels
                                                                                                         Dolphin GT;
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                                                                                                     Baltzer L,
                                                                                                                                                                                                          Claim 18; Page 75; 102pp; English.
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                                                                                                     Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95.8%;
91.7%;
            98SE-0002441.
98SE-0002562.
98SE-0004614.
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                                                                         (ASCI-) A+ SCI INVEST AB.
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nes 11; Conserv
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                           17-JUL-1998;
29-DEC-1998;
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                                                                                                       Hanson LA,
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AAY78001 to AAY78100 represent peptides having sequences based on human latter actoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such and and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                The agent is low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infections,
               AAR98531-54 are peptides used in an anti-ulcer agent. The a
in toxicity, is heat-resistant and stable in aqueous soln..
administered orally and be produced in large amounts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                        Length 15;
                                                                                                                    95.8%; Score 68; DB 17; Length 15
91.7%; Pred. No. 5.5e-05;
ive 1; Mismatches 0; Indels
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                                                                                                                                                          11; Conservative
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                                                                                                                                         Local Similarity
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                                                                                    15 AA;
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                                                                                      Sequence
                                                                                                                    Query Match
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Sequence

AAY78063 standard; Peptide; 15 AA.

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25-APR-2000 (first entry)

AAY78063;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
                                                                                                                                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; uninary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                             Gaps
                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
   95.8%; Score 68; DB 21; Length 15; 91.7%; Pred. No. 5.5e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95.8%; Score 68; DB 21; Length 15; 91.7%; Pred. No. 5.5e-05; ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dolphin GT;
                                                                                                                                                                                                                                                                                      Human lactoferrin derived peptide SEQ ID NO:62.
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                                                                                                                                                                                     AAY78062 standard, Peptide, 15 AA.
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98SE-0004614.
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                                                                                                                                                                                                                                                        (first entry)
                                      11; Conservative
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                                                                                                    4 CFOWORNMRKVR 15
                                                                   1 CFQWERNMRKVR 12
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Query Match
Best Local Similarity
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Best Local Similarity
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29-DEC-1998;
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Synthetic.
                                                                                                                                                                                                                       AAY78062;
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                    Best Loca
Matches
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would costs.
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                                                                                                                          Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 68; DB 21; Length 15; Pred. No. 5.5e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dolphin GT;
                                                                                           Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 18; Page 81; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                   98SE-0004614.
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91.7%;
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Best Local Similarity 91.77
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 AA;
                                                                                                                                                                                                                                                     WO200001730-A1.
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29-DEC-1998;
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                                                                                                                                                                                                                         Synthetic.
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Gaps

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11; Conservative

Matches

4 CFÓWQRNMRKVR 15

CFOWERNMRKVR 12

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Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urlnary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                         Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                Hanson LA, Mattsby-Baltzer I,
        25-APR-2000 (first entry)
                                                                                                                                                                                               (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                 WPI; 2000-147388/13.
                                                                                                             WO200001730-A1.
                                                                                     Homo sapiens.
                                                                                                                                                                      17-JUL-1998;
29-DEC-1998;
                                                                                                                                              06-JUL-1999;
                                                                                                                                                             06-JUL-1998;
                                                                                                                             13-JAN-2000.
                                                                                             Synthetic.
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98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

Baltzer L, Dolphin GT;

16 AA; Sequence

1 CFOWERNMRKVR 12 셤

Search completed: February 21, 2003, 07:37:15 Job time : 29.35 secs

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the spetide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammarions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower Claim 11; Page 68; 102pp; English.

Query Match 95.8%; Score 68; DB 21; Length 16; Best Local Similarity 91.7%; Pred. No. 5.9e-05; Matches 11; Conservative 1; Mismatches 0; Indels

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0; Gaps

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LOCATION: 1.18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Peptide
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Sequence 30,
Sequence 29,
Sequence 6, A
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Sequence 24,
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Sequence 24
Sequence 25
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Sequence 8,
Sequence 8,
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Sequence 6
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Sequence 8
Sequence 8
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.3
(c) 1993 - 2003 Compugen Ltd.
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US-08-465-948-8

US-08-475-055-8

US-07-951-174-3

US-07-91-174-3

US-08-256-771-24

US-08-256-771-24

US-08-381-984-25

US-08-381-984-25

US-08-381-984-25

US-08-381-984-25

US-08-381-984-25

US-09-508-734-4

US-09-508-734-8

US-09-508-734-8

US-08-256-771-30

US-08-256-771-30

US-08-256-771-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

US-08-464-182A-6

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US-08-464-182A-6
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Maximum Match 100%
Listing first 45 summaries
                                    - protein search, using sw model
                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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71
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Match Length
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Perfect score:
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US-08-464-182h-2 US-08-406-271-2 US-08-724-586-2 US-09-471-632-2 US-08-655-640-2 US-08-655-640-4 US-08-655-640-4 US-08-655-640-4 US-08-655-640-4 US-08-655-640-4	476-798 145-681 250-308 455-106- 265-577-	ALIGNMENTS	ON AND PROTECTA, 1
US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08- US-08-	-80-80 US-08- US-08- US-08- US-08- US-08- US-08-	ALI	1. Lication US/08204487 4.425 YAMAMOTO, NAOXI NAKASHIAM, HIDEKI NAKASHIAM, HIDEKI NAKASHIAM, HIDEKI NAKASHIAM, HIDEKI NAKASHIAN, USHARAKI TANAKA, SHIGEAKI DOSAKO, SHUN'ICHI TANAKA, TOSHIAIN OUTHOR, TOSHIAIN OUTHOR, TOSHIAIN SENTION: INHIBITORS GUENCES: 8 CE ADDRESS: PATENT ADMINISTRATOR, TESTP THIBEAULT 3 STATE STRET TON STATE STRET TON USA DABLE FORM: E: Floppy disk IEM PC Compatible SYSTEM: PC-DOS/MS-DOS PATENTIN RElease #1.0, Versi IEM PC Compatible SYSTEM: US/08/204,487 TION: SI4 TION: S14 TION: S17 TION: S18 TION: S17 TION: S
なるますみなるましきす			I US/082044 I US/082044 MATANU SHIGGAKI SHUN'ICHI VIRAL INF INHIBITOR SS: SS: ADMINISTR STRET ST
5 4 4 6 6 9 4 4 6 9 6 9 4 4 6 9 9 4 4 6 9 9 9 9	7117		Application US/082044 5565425 11: YAMAMOTO, NAOKI 12: YAMAMOTO, NAOKI 13: NAKASHIMA, HIDEKT 13: DOSAKO, SHUN'ICHI 14: TANAKA, SHIGEAKI 15: DOSAKO, SHUN'ICHI 17: KAMASAKI YOSHIHRE 17: UCHIDA, TOSHIHRE 17: UCHIDA, TOSHIHRE 18: UCHIDA, TOSHIHRE 18: TANAKAKI YOSHIHRE 18: UCHIDA, TOSHIHRE 18: TANAKAKI YOSHIHRE 18: TANAKAKI YOSHIHRE 18: TANAKAKI AMINISTR 18: TANAKAKI AMINISTR 18: TANAKANISTR 18: TANAKANISTR 18: TANAKANISTR 19: TANAKANISTR 10: USA 12: USA 13: USA 13: USA 13: USA 13: USA 14: USA 15: USA 16: USA 17: USA 1
	90.00 91.00 91.00 91.00 91.00 91.00		3, Application 3, Application 20, 5565425 CANT: YAMAMOTO, CANT: YAMAMOTO, CANT: WAKASHIMA CANT: MAKASHIMA CANT: MAKASAKI CANT: MAKASAKI CANT: MAKASAKI CANT: MAKASAKI CANT: MAKASAKI CANT: MAMASAKI CANT: MAMASAKI CANT: MAKASAKI CANT: MAKASAKI CANT: MAKASHIMA CANTIMA CANTIMA CANTIMA CANTI
			SULT 1 Sequence 3, Application US/0820448: Patent No. 556545. GENERAL INFORMATION: APPLICANT: VAMAMOTO, NAOKI APPLICANT: VARASHIMA, HIDEKI APPLICANT: TANAKA, SHIGBAKI APPLICANT: TANAKA, SHIGBAKI APPLICANT: TANAKA, SHIGBAKI APPLICANT: TANAKA, SHUM-ICHI APPLICANT: UCHIDA, TOSHIHIRO APPLICANT: USA CITY: BOSTON STATE: MA COUNTRY: USA ZIP: CITY: BOSTON COMPUTER: IBM PC COMPATION COMPUTER: IBM PC COMPATION COMPUTER: IBM PC COMPATION COMPUTER: IBM PC COMPATION APPLICATION NUMBER: US/08/204 FILING DATE: TO2-MAR-1994 CLASSIFICATION NUMBER: US/08/204 FILING DATE: APPLICATION NUMBER: FIN- TELEPHONE: (G17) 248-7100 TELEPHONE: (G17) 248-7100 TELEPHONE: (G17) 248-7100 TELEPHONE: (G17) 248-7100 TELEFAX: G17) ARBILL TYPE: Amino acids TYPE: Amino acids TYPE: Amino acids TYPE: Amino acids TYPE: Innear
	6 6 4 4 4 4 4 6 0 C C C C C C C C C C C C C C C C C C		RESULT US-08-7 US-08-7 US-08-7 AP
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us-09-743-107b-84.rai

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Sequence 8, Application US/08628380
Patent No. 5891341
GENERAL INFORMATION:
APPLICANT: LI, YONG MING
APPLICANT: VIASSARA, HELEN
APPLICANT: CERAMI, ANTHONY
TITLE OF INVENTION: AGE-MEDIATED INHIBITION OF ANTIBACTERIAL PROTEINS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: APPLII 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: JACKSON ESQ., DAVIG A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008 CIP
TELEPHONE: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-475-055-8; Sequence 8, Application US/08475055 Patent No. 596245; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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; FRAGMENT TYPE: internal
US-08-628-380-8
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STRANDEDNESS: si
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                                                                                                         US-08-628-380-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HIGHAN VIASSARA
APPLICANT: HIGHON VIASSARA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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                                                                                           Query Match
95.8%; Score 68; DB 1; Length 18;
Best Local Similarity 91.7%; Pred. No. 4e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION DATA:
FILING DATA:
CLASSIFICATION: 436
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APPLICATION: 436
APPLICATION NUMBER: 08/418,642
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAWE: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 947-1-008A
TELEPOME: 201 487-5800
TELEPOME: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR ESQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPEN E AMINO ACIDS
TYPEN E
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8, Application US/08485948
Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
OTHER INFORMATION: (20-37)"
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MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FRAGMENT TYPE: internal US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                        1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                   1 CFOWORNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
             ;
US-08-204-487-3
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APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: ARGUNTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
95.8%; Score 68; DB 2; Length 18; 91.7%; Pred. No. 4e-05;
                                                         1; Mismatches
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1 CFOWORNMRKVR 12

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NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified site
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95.8%; Score 68; DB 1; Length 20;
  OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTONNEY, AGENT INFORMATION:
NAME: WARTEN INFORMATION:
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOCUMENT NUMBER:
PILING DATE:
PRILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
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CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
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ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VOLUME:
ISSUE:
PAGES:
                                                                                                                                                                                                                                                                                                                                         TELEX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/07755161A
Patent No. 5304633
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREE: 805 Fifteenth Street, N.W., #700
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                 ZIP: 07601

ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                PRIOR APPLICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/485,948
FILING DATE: 08/488,217
FILING DATE: 1018 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELEPHONE: 201 487-5800
TELEPAX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHRACATERISTICS:
                   E: Klauber & Jackson
411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 95.8
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-475-055-8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                       CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                          FILING DATE:
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DENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: (ys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
DENTIFICATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
PUBLICATION INFORMATION: thiol group of Cys residue at location 2"
AUTHORS:
AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHICERALI
APPLICANT: TANAKA, SHICERALI
APPLICANT: TANAKA, SHICERALI
APPLICANT: KAWASAKI, YOSHINIRO
APPLICANT: UNUBNIION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: IMHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO comparible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
TURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
APPLICANT: YAMANOTO, NAOKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               DOCUMENT NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 02109
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STREET: 53
                                                                                                                                                                                                                                                                                                                                     JOURNAL:
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US-08-204-487-1
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US-07-891-174-3

i Sequence 3, Application US/07891174

i Patent No. 517084

i GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

ITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: ADDRESSE:

ADDRESSEE: ADDRESSE:

ADDRESSEE: Wenderoth Lind & Ponack

MUMANIAN AND ADDRESSE:

ADDRESSEE: Wenderoth Lind & Ponack

ADDRESSEE: Wenderoth Lind & W. # 4700
    Pred. No. 4.4e-05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: M5-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION TOWNER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENI INFORMATION:
NAMME: WARTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: modified site
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                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                          2 CFQWQRNMRKVR 13
                                                                 1 CFQWERNMRKVR 12
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CHROMOSOME/SEGMENT;
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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FRAGMENT TYPE:
ORIGINAL SOURCE:
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RESULT >
US-08-256-771-25

US-08-256-771-25

Sequence 25, Application US/08256771

Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

95.8%; Score 68; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.4e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match

95.8%; Score 68; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4.4e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: peptide FEATURE:
                                                                                                                        1 CFQWERNMRKVR 12
                                                                                                                                          2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CFQWQRNMRKVR 13
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                US-08-256-771-24
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US-08-381-984-24
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APPLICANT: Mamoun TOMITA et al.

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fitteenth Street, N.W., #700
CITY. Mashington
                                                                                                                                                                                                                                                                Query Match 95.8%; Score 68; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4.4e-05; Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                           LOCATION: 1.20
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IEM Compatible OFBRATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
CLASSIPPICATION: 514
PRIOR APPLICATION: 514
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 24, Application US/08256771
Patent No. 5656591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORREY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24:
TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : 20 amino acids
amino acid
                                                                                            single
                                                                                                                        MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                            NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                          2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                     1 CFOWERNMRKVR 12
                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
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                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
US-08-256-771-24
                                                                                                                                                                                                                                 US-08-204-487-1
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Gaps

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us-09-743-107b-84.rai

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OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment therec
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TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PASSYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR PRILING DATE: 1999-07-14
PRIOR FILING DATE: 1998-07-14
PRIOR PILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | IDENTIFICATION METHOD:
| OTHER INFORMATION: /note= "cysteine residues at positions 2
| OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
| US-08-381-984-25
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                                                                                                                                                   MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
ODERATING SYGTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFFCATION: 252
PRICAR APPLICATION NUMBER:
APPLICATION NUMBER:
                 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
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US-09-508-734-4
; Sequence 4, Application US/09508734
; Patent No. 6423509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 amino acids
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IDENTIFICATION METHOD:
                                                                                                                                  COMPUTER READABLE FORM:
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                                    Washington
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                                                                                      U.S.A.
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                                                                                   COUNTRY:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thered
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                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: WORDPEFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/381,984 FILING DATE: APPLICATION: 252 PRIOR APPLICATION: 252 PRIOR APPLICATION DATA: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER:
                                                             TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoch, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
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Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
INTRES OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
Sequence 24, Application US/08381984 Patent No. 5804555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
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IDENTIFICATION METHOD:
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MOLECULE TYPE: peptide
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                                            GENERAL INFORMATION:
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Matches
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LOCATION: 21
IDBNITECTATION METHOD: 0
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" sublication: AUTHORS:
AUTHORS:
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LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
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95.8%; Score 68; DB 1; Length 25;
Best Local Similarity 91.7%; Pred. No. 5.5e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
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RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                        REFERENCE/DOCKET NUMBER:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-311-8850
TELEPAX: 202-371-8856
                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: modified gite
                                                                                                                                                                                                                                                                                                                                                                                                                 single
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CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION:
CHROMOSONE/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ANTI-SENSE;
FRAGMENT TYPE;
ORIGINAL SOURCE;
ORGANISM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11;
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
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VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN:
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                                                                                                                                                                                                                                                                                                                                                                                                                          USCOURT (1.20) 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1.00 | 1
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0
                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                    ó
                                                                                                                                        Query Match
95.8%; Score 68; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 4.9e-05;
Matches 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95.8%; Score 68; DB 4; Length 24; 91.7%; Pred. No. 5.3e-05; Live 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/07755161A

Batent No. 5304633

GENERAL INFORMATION:
APPLICAMT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM COMpatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER;
                        TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                                                                         1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 CFQWQRNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.C.
(: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-07-755-161A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D
                                                                                     US-09-508-734-4
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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/note= "thiol group of
Cys residue at location 4 connected by disulfide bond with
thiol group of Cys residue at location 21"
RESULT 15
US-07-891-74-10
Sequence 10, Application US/07891174
Sequence 10, Application US/07891174
Setulation US/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: M5-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Displaykrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION S30
PRIOR APPLICATION DATA:
APPLICATION WHER: US/07/55,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECHONNINICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELECHOMUNICATION INFORMATION:
TELECHOME: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL: AMII-SENSE: FRAGMENT TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 4
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
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NAME/KEY: modified site LOCATION: 21

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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                         / Match 95.8%; Score 68; DB 1; Length 25; Local Similarity 91.7%; Pred. No. 5.5e-05; Nes 11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Search completed: February 21, 2003, 07:50:36 Job time : 8.7 secs
                                                                                                                                                                                                                                                                DOCUMENT NUMBER:
FILING DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 CFÓWQRNMRKVR 15
                                                                                                                                                                                                                                                                                                                                                  US-07-891-174-10
                                                                                                                                                                JOURNAL:
                                                                                                                                                                                      VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                         PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Sequence 30, Appl
Sequence 2, Appli
Sequence 4, Appli
Sequence 47985, A
Sequence 46393, A
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Sequence 26, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 119, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Appl
Sequence 20, App
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 29, Appl
                                                                                              February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 30,
Sequence 2, 1
Sequence 4, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4
Sequence 2
Sequence 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications AA:*

1: cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/NEON_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/pubpaa/US60_NEW PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBGOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-864-761-47985
US-09-864-761-46393
US-09-738-626-5715
US-09-796-753-26
US-09-978-295A-119
                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-798-869-2
US-09-798-869-2
US-00-798-869-6
US-09-798-869-3
US-09-798-869-3
US-09-798-869-4
US-09-798-869-4
US-09-798-869-2
US-09-798-869-2
US-09-798-869-2
US-09-798-869-29
US-09-798-869-29
US-09-788-869-29
US-09-788-869-30
US-09-888-30-29
US-09-888-30-29
US-09-888-30-30
                                                                                                                                                                                                                                                                                  156504 segs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                 US-09-743-107B-84
71
                                                                                                                                                                                                  1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perfect score:
                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                                                                                                                                                 Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Result
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Sequence 530, App	US-09-925-302-530	10	168	46.5	e e	45
1031,	US-09-764-864-1031	10		46.5	33	44
	US-09-764-869-1200	10	88	46.5	33	43
e 410	US-09-864-761-41002	10	77	46.5	33	42
58,	US-10-066-494-58	σ	747	47.9	34	41
Sequence 58, Appl	US-10-066-273-58	σ	747	47.9	34	40
58,	US-10-002-796-58	თ	747	47.9	34	6 6
Sequence 58, Appl	US-10-066-500-58	σ	747	47.9		38
Sequence 1324, Ap	US-09-925-300-1324	10	248	47.9	34	3.7
Sequence 33619, A	US-09-864-761-33619	10	99	47.9	34	36
Sequence 320. App	US-09-984-245-320	σ	63	47.9	34	32
Sequence 13026. A	US-09-815-242-13026	10	62	47.9		34
	US-09-815-242-12129	10	62	47.9		33
Sequence 46806. A	US-09-864-761-46806	10	20	47.9	34	32
	US-09-963-959-2	σ	1701	49.3	35	31
Sequence 28, Appl	US-09-981-649A-28	10	559	49.3	35	30
	US-09-981-649A-32	10	554		35	29
		10	554		35	28
		10	553	49.3	32	27
Sequence 6, Appli	US-09-981-649A-6	70	553	•	32	26
14	US-09-796-753-14	σ	553		35	25
œ	US-09-989-861-8	10	388		35	24
119	US-09-978-189-119	σ	338	•	35	23
Sequence 119, App	US-09-999-832A-119	თ	338	•	32	22
	US-09-978-192A-119	σ	338	49.3	35	21
Sequence 119. App	US-09-978-697-119	ø,	338	49.3	35	20

RESULT 1
US-09-798-869-2
US-09-798-869-2
Sequence 2, Application US/09798869
Fublication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: (YSTEIN REXDAL
APPLICANT: ASTEIN REXDAL
TITLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT PILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
PRIOR FILING DATE: 1998-08-28
SOFTWARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 15
TYPE: RRT

ALIGNMENTS

Query Match 95.8%; Score 68; DB 9; Length 15; Best Local Similarity 91.7%; Pred. No. 3.6e-05; Matches 11; Conservative 1; Mismatches 0; Indels 0;

US-09-798-869-2

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Gaps

OY 1 CFOWERNMRKVR 12 | | | | | | | | | | | Db 3 CFOWORNMRKVR 14 VS-09-798-869-20
Sequence 20, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: ASLDUR SVEINBJ RESCON
APPLICANT: BALDUR SVEINBJ RESCON

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Patent No. US20020160941A1
GENERAL INFORMATION:
APPLICANT: Kurecki, Tomasz
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
APPLICANT: OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoférrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                COUNTY: Washington D.C.

ZIP: Z0004

ZIP: Z0004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A.
                TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
RICK FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE DOCKET NUMBER: 10505/P58185C
TELECOMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
PADLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
  LARS VORLAND
                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 CFÓWQRNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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US-10-023-096-2
                                                                                                                                                                                                                                                   SEQ ID NO 20
LENGTH: 25
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APPLICANT:
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                                                         Gaps
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                                                       0;
           Length 694;
  95.8%; Score 68; DB 9; Length 694
91.7%; Pred. No. 0.0014;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 84.5%; Score 60; DB 9; Length 15;
1 Similarity 83.3%; Pred. No. 0.0007;
10; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 51; DB 9; Length 15; Pred. No. 0.02;
                                                                                                                                                                                                                                                                                                                  APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: ALALDY SVEINBAL (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BICACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR PLING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSEISEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: BIOACHIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: RastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                      Sequence 6, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09798869
Publication No. US2030022821A1
SENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: RYTERIN REKDAL
APPLICANT: BALDUR SVENIBJ (RNSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.8%;
63.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                               11; Conservative
Query Match
Best Local Similarity
                                                                                             1 CFOWERNMRKVR 12
                                                                                                                                        22 CPOWORNMRKVR 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWERNMRKVR 12
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Best Local Similarity
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Best Local Similarity
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; ORGANISM: CAPRINE
US-09-798-869-3
                                                                                                                                                                                                           RESULT 4
US-09-798-869-6
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US-09-798-869-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
                                               Matches
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0
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; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                  1 CFOWERNMRKV 11
                                                  3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 CLRWQNEMRKV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWERNMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: MURINE
US-09-798-869-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: MURINE
US-09-798-869-22
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US-09-798-869-22
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LENGTH: 25
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          0; Gaps
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US-09-798-869-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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        1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 60.6%; Score 43; DB 9; Length 15; Best Local Similarity 54.5%; Pred. No. 0.38; Matches 6; Conservative 3; Mismatches 2; Indels
      3; Mismatches
                                                                                                                                                                  Sequence 33, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OCHN SIGURD SVENDSEN
APPLICANT: ARS YORLAND
APPLICANT: ARS YORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRERENCE: A34649-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRANCES OF SEC EV Mindows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7, Application US/09798869
Publication No. USZ0030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGGED SYENDSEN
APPLICANT: HALDUR SYENBER (NSSON
APPLICANT: HALDUR SYENBER (NSSON
APPLICANT: LARS VORLAND:
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFREENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,669
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 63.6
Matches 7; Conservative
                                        1 CFOWERNMRKV 11
                                                                             3 CYOWORRMRKL 13
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3 CYQWQRRMRKL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                                                      US-09-798-869-23
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59.2%; Score 42; DB 9; Length 25; 54.5%; Pred. No. 0.9; 1ve 2; Mismatches 3; Indels
US-09-798-869-4

Sequence 4, Application US/09798869

Publication No. US20030022821A1

GENERAL INFORMATION:
APPLICANT: JCHN SIGUED SVENDEN

APPLICANT: GYSTEIN RENDAL

APPLICANT: HYSTEN SPENDEL

APPLICANT: LARS VORLAND

TITLE REPERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FRSELSEQ FOR Windows Version 4.0

SEQ ID NO 4

LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYBINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRAESEQ for Windows Version 4.0
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APPLICANT: Barry III, Clifton E.
APPLICANT: Barry III, Clifton E.
APPLICANT: Barry III, Chisimuzi.
APPLICANT: Mdlul, Khisimuzi.
APPLICANT: Mdlul, Khisimuzi.
APPLICANT: Mdlul, Khisimuzi.
APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
ITILE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
CURRENT FILING DATE: 2001-06-22
FRIOR APPLICATION NUMBER: US 60/214,187
FRIOR APPLICATION NUMBER: US 60/214,187
FRIOR FILING DATE: 2000-06-26
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ) ORGANISM: Mycobacterium tuberculosis
) OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.9%; Score 39; DB 9; Length 15; 45.5%; Pred. No. 1.7; 2; Indels Live 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.5%; Score 38; DB 9; Length 489; 54.5%; Pred. No. 67; tive 2; Mismatches 3; Indels
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: OTHER SIGNED
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 30
LENGTH: 15
LENGTH: 15
LENGTH: 15
RECORD NOS: 30
SEQ ID NO 30
LENGTH: 15
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; Publication No. US20030013090A1
; GENERAL INFORMATION:
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US-10-051-409-4
Sequence 4, Application US/10051409
Publication No. US20030027171A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWERNMRKV 11
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: BOVINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-798-869-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine ; OTHER INFORMATION: sequence)
US-09-798-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ilarity 54.9%; Score 39; DB 9; Length 15; S4.5%; Pred. No. 1.7; Conservative 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.9%; Score 39; DB 9; Length 15; 45.5%; Pred. No. 1.7; tive 4; Mismatches 2; Indels
                                                                                                                                                  APPLICANT: LEJELIN KEALMAL

APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE EFFTIDES
FILLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILLING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: CT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILLING DATE: 1998-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELSEQ FOR WINDOWS Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29, Application US/09798869
Fublication No. US20030022821A1
GENERAL INPORMATION:
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/G899/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
                                   Sequence 8, Application US/09798869; Publication No. US20030022821A1
                                                                                                              APPLICANT: JOHN SIGURD SVENDSEN APPLICANT: (YSTEIN REXDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Seguence
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Best Local Similarity 45.5
Matches 5; Conservative
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Best Local Similarity
....hes 6; Conserva
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                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: BOVINE
US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-798-869-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 8
LENGTH: 15
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Dp

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Gaps

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Gaps

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RESULT 12 US-09-798-869-30

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TYPE: PRT
ORGANISM: Homo sapiens
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LENGTH: 21
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Setent No. US202004975A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Hand, Sharron G.
TITLE OF INVENTION: HUMAN EXPRESSION ANALYSIS BY MICROARRAY
CUMRENT APPLICATION WINBER: US/09/664,761
PRIOR PAPLICATION WINBER: US/09/664,761
PRIOR APPLICATION WINBER: US/09/664,761
PRIOR PAPLICATION WINBER: US/01-05-23-6
PRIOR APPLICATION WINBER: US/01-06-03-24-66
PRIOR APPLICANTON WINBER: US/01-06-03-24-66
PRIOR APPLICANTON WINBER: PCT/VS01/00666
PRIOR APPLICANTON WINBER: PCT/VS01/00666
PRIOR APPLICANTON WINBER: PCT/VS01/00666
PRIOR APPLICANTON WINBER: PCT/VS01/00669
PRIOR PRIOR APPLICANTON WINBER: PCT/VS01/00669
PRIOR PRIOR APPLICANTON WINBER: PCT/US01/00669
PRIOR PRIOR PAPLICANTON WINBER: PCT/US01/00661
PRIOR PLING DATE: 2001-01-30
PRIOR PLING PLING DATE: 2001-01-30
PRIOR PLING PLING DATE: 2001-01-30
PRIOR PLING PLING DATE
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                                                                                         APPLICANT: Fann, Ming-Ji
APPLICANT: Chou, Chen-Kung
TITLE OF INVENTION: CELL CYCLE REGULATOR PROTEIN
FILE REFERENCE: 12005-003001
                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/051,409
CURRENT FILING DATE: 2002-01-18
PRIOR PILING DATE: 2002-01-18
PRIOR FILING DATE: 2001-01-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASISEQ for Windows Version 4.0
LENGTH: 846
Yang, Chu-Wen
Tsou, Ann-Ping
Chi, Chin-Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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Matches 4; Conserv
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448 CFEWDRKL 455
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US-09-864-761-47985
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-84 Title: Perfect score:

1 CFQWERNMRKVR 12 Sequence:

Scoring table:

283224 seqs, 96134422 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:* Database

pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cri	Antion A	lactoferrin - goat	1	5		26S protessome SII	thetical	11.4		abolinonrotein B-1		himothetical prote		MHC Class T histoc	יי קייר	trimethylemine N-0	3-deoxy-manno-ooth	hypothetical prote	probable cytochrom	probable monooxyge	CVTOChrome P450-11		D450-	DAED	יייב הייב הייב	1 -	1 -	4 -	pyridoxamine 5'-ph
SUMMARIES	QI	TEHUL	JC2323	852107	AB0858	A28438	E90094	T22597	B85431	T08030	B60950	G86403	T29571	AD2346	137477	A45687	G82168	D71876	T32605	B96691	C70655	B85441	T04730	C85441	T52174	C84325	551	T28820	B64485	745
	DB	1															7	7	7	7	Ŋ	7	7	7	0	7	0	N	~	0
	Length	711	708	33	511	707	205	275	1432	4568	274	289	361	298	365	749	820	393	433	481	489	492	499	200	500	584	887	932	S	206
ф	Query Match		ä	7	62.0	59.2	57.7	57.7	57.7	57.7	56.3	56.3	56.3	54.9	54.9	54.9	54.9	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	53.5	52.1	52.1
	Score	68	51	48	44	42	41	41	41	41									38											
	Result No.	-1	7	е	4	Ľ	9	7	00	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

pyridoxamine 5'-ph probable pyridoxam	signal peptidase I cathepsin L (EC 3.	cathepsin L (EC 3. probable tyrosine	cytochrome P450 (E	tyrochrone pass = hypothetical prote	hypothetical prote	Hypolnetical profe F1511.22 [imported	probable secreted	probable oxidoredu	protein sam2B - sp	nypotnetical prote
AB2670 AG3441	E87515 KHRTL	KHMSL C71467	T10896 F71417	T24218	T19429	C96582	B87162	E70848	10921/	614069
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52.1	52.1	52.1 52.1	52.1	52.1	52.1	50.7	50.7	50.7		
37	37.	37	37	37	37	36	36	3.6	9 0)
30	333	2. E.	36 37	38	3.9 4.0	41	42	4 4 4 4	, 4	1

ALIGNMENTS

RESULT 1

	TFHUL
	lactotransferrin precursor (validated) - human
	N;Alternate names: lactoferrin
_	C; Species: Homo sapiens (man)
_	C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #rext change 08-Dec_2000
_	C; Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; S21160; S21160; S21160
	R;Cho, Y.
	submitted to the EMBL Data Library. March 1994
	A;Reference number: G06820
_	A; Accession: G01394
	A; Status: preliminary; translated from GB/EMB1. Ind.
	A; Molecule type: mRNA
	A; Residues: 1-711 <cho></cho>
_	A; Cross-references: EMBL: U07643; NID: 9467236; PIDN: AAB60324.1; PID: 6467237
	R; Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
	Nucleic Acids Res. 18, 5288, 1990
	A; Title: Complete nucleotide sequence of human mammary gland lactoferrin
	A; Reference number: S11228; MUID: 90384839; PMID: 2402455
	A; Accession: S11228
	A; Molecule type: mRNA
	A; Residues: 1-148,'T',150-422,'C',424-711 <rey></rey>

A)Cross-references: EMBL:X53961; NID:g34415; PIDN:CAA37914.1; PID:g34416
R)Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A;Title: Differential molecular mechanism of the estrogen action that regulates lactofer;
A;Reference number: A45401; MUID:93125571; PMID:1480183

A; Molecule type: mRNA A; Residues: 3-711 <POW> A; Residues: 3-711 <POW> A; Cross-references: BHD::X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412 R; Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W. Biochem. J. 276, 349-355, 1991 A; Title: Expression of cloned human lactoferrin in baby-hamster kidney cells. A; Reference number: S15853; MUID:91264786; PMID:2049066

A; Status: nucleic acid sequence not shown; not compared with conceptual translation

A,Molecule type: mRNA A,Residues: 20-31 <ST1> A,Accession: 820841 A,Molecule type: protein A,Residues: 20-28,'X',30-31 <ST2>

; 0

Gaps

.

1; Indels

Length 708

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Biochim. Biophys. Acta 1243, 25-32, 1995
AyTitle: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet & A;Reference number: $52107; WUID:95127729; PMID:7827104
A;Accession: $52107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gispecies: Salmonella enterica subsp. enterica servar Typhi A.Note: this species has also been called Salmonella typhi Gibate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 Gibate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 Riparkhili, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Connerton, P.; Cronin, A.; Davis, P.; Daviss, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A.Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A; Reference number: AB0502; PMID:11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-511 <PAR>
A;Cross_references: GB:AL513382; PIDN:CAD06049.1; PID:g16504016; GSPDB:GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z_Y;,Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N'Alternate names: lactotransferrin
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.6%; Score 48; DB 2; Length 33; 54.5%; Pred. No. 0.067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: protein
A;Residues: 1-33 «QIA»
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
                                            DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62.0%; Score 44; DB 2; 58.3%; Pred. No. 5.7;
                                     Score 51; DB
Pred. No. 0.46
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                 71.8%;
63.6%;
Query Match
Best Local Similarity 63.67
Electron 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              lactoferrin - sheep (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           350 CFAWDMNKAKVR 361
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Matches 6; Conserva
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                                                                                                                                                                               1 CFQWERNMRKV 11
                                                                                                                                                                                                                                               38 CYQWQRRMRKL 48
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                                                                                                                                                                                       A; Residues: 436-487, 'A', 489-711 <RAD>
A; Ross-references: EXBL:MM8642; NID:g186815; PIDN:AAA86665.1; PID:g386855
A; Cross-references: EXBL:Mm8642; NID:g186815; PIDN:AAA86665.1; PID:g386855
B; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043; 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                      A)Status: not compared with conceptual translation
A;Nolecule type: mRNA
A;Molecule type: mRNA
A;Residues: 3-701, SWRPWY <PAN>
A;Experimental source: normal breast tissue
B;Experimental source: Mazurier, J; Schoentgen, F; Legrand, D; Spik, G;
By Title: Human lactorransferrin: amino acid sequence and structural comparisons with oth
A;Reference number: A31000; MUID:85076667; PMID:6510420
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C,Superfamily: transferrin; transferrin repeat homology
C,Superfamily: transferrin; transferrin; iron binding; milk
E;Leywords: duplication; glyoptotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRH1>
F;240-65/Domain: transferrin repeat homology <TRH1>
F;240-65,135-218.177-133,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F:157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
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R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Blophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A;Reference number: JC2323; MUID:94380047; PMID:8093048
A;Reference number: JC2323; MUID:94380047; PMID:8093048
A;Redevale type: mRNA
A;Residues: 1-708 <LED>
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; alyoprotein
F;359-696/Domain: transferrin repeat homology 

F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A;Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A;Note: this is the final paper in a series
B;Note: this is the final paper in a series
B;Notem, G.; Hoegdall, B.V.; Barkholt, V.; Norskov, L.

Bur. J. Biochem. 241, 303-308, 1996
A;Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affinal arkeference number: S74119; MUID:97054624; PMID:8898921
              Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
A;Accession: S07160
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C;Date: 20-Feb.1995 #8equence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GDB:119368; OMIM:150210
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91.7%;
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Best Local Similarity
                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: A61169
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A;Gene: ODA4
A;Gene: ODA4
A;Gene: ODA4
A;Gene: ODA5
A;Gene: ODA6
A;Map position: IX
A;Into R: 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 1
3334/3; 3686/3; 3882/3; 4246/3
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nuclectide binding; P-loop
F;1919-1926/Region: nuclectide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Accession: B85431
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sprin
Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
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CiDate: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
CiAccession: T0830
Rimitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
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A,Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A,Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A.Residues: 1-1432 <STO>
A.Gross-references: GB:NC_001268; NID:97270600; PIDN:CAB80318.1; GSPDB:GN00140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
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A, Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
C, Genetics: C, Genetics: Strain 21gr
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A,Introns: 67/1; 153/1
C,Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                    57.7%; Score 41; DB 2; Length 275; 63.6%; Pred. No. 10; 2; Indels ative 2; Mismatches 2; Indels
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                                                  A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: DNA
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A, Status: translated from GB/EMBL/DDBJ
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54.5%;
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Matches 7; Conservative
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Matches 6; Conservative
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                            A; Accession: T22597
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                         R/Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139, 1987
A/Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
A/Reference number: A92596; MUID:87280033; PMID:3611056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 24-May-2001
C;Accession: E90094
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Rei
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671
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A;Cross-references: GB:AF165818; NID:913794510; PIDN:AAK39885.1; GSPDB:GN00150
                                                                                                                                                                                                                                         Riliu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
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C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C.Accession: T22597
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Pred. No. 18;
2; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fil-19/Domain: signal sequence #status predicted <SIG>Fi20-707/Product: lactotransferrin #status predicted <MAT>Fi3S8-695/Domain: transferrin repeat homology <TRH2>
                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-15 <LIU>
A;Cross-references: GB:M74778
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
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                                                                                                                                                                                                                  Cross-references: EMBL:J03298
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Best Local Similarity 75.00
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C; Accession: A28438; A41205
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37 CLRWQNEMRKV 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWERNMRKV 11
                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 3-707 <PEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Gene: prsB5
A;Map position: 1
A;Genome: nucleomorph
C;Keywords: nucleomorph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: E90094
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 CFFWERNL 70
                                                                                                                                      A; Accession: A28438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                         Accession: A41205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches

C; Genetics:

ð

Matches

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Cispecies: Nostoc sp.
Abyote: Nostoc sp.
Abyote: Nostoc sp.
Abyote: Nostoc sp.
Cirain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
Cidate: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
Cidatession: AD2346
Cidatession: AD246
Cidatession: AD346
Cidatession: AD346
Cidatession: AD346
Cidatession: AD346
Cidatession: AD346
Cidatession: AD346
Cidatession: Apimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, Subakases et al. 205-213, 2001
A;Tile: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium AnsayReference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WHC class I histocompatibility antigen alpha chain HLA-A34 precursor - human C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Oc. 2-01-1396 #sequence revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: 13497; S16711; S16771
R;Madrigal, J.A.; Bellch, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour, J. Immunol. 149, 3411-3415, 1992
A;Title: Distinctive HLA-A, B antigens of black populations formed by interallelic converses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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A;Residues: 1-298 «KUR»
A;Cross-references: GB:BA000019; PIDN:BAB76022.1; PID:g17133459; GSPDB:GN00179
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: a1r4323
                                                                            Cispecies: Caenorhabditis elegans
Cibate: 15-0ct-1999 #sequence_revision 15-0ct-1999 #text_change 04-Mar-2000
Ciaccession: T29571
RiMiller, N.; Bradshaw, H.
Submitted to the EMBL Data Library, December 1995
A;Description: The sequence of C. elegans cosmid F30B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Gene: CES9:F30B5.4
A.Introns: 140/3; 179/2; 223/1
C.Superfamily: Caenorhabditis elegans hypothetical protein F30B5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                56.3%; Score 40; DB 2; Length 361; 60.0%; Pred. No. 20; Live. 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-361 <MIL>
A;Residues: 1-361 <MIL>
A;Cross-references: EMBL:U42437; PIDN:AAA83493.1; CESP:F30B5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 39; DB 2; Length 298;
Pred. No. 25;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: 137476; MUID:93056508; PMID:1431115
A; Accession: 137477
                                                         hypothetical protein F30B5.4 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-365 <RES>
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Best Local Similarity 66.7°
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWERNMRK 10
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A,Note: authors translated the codon ATA for residue 8 as Val
C,Superfamily: apolipoprotein B
C,Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                I DI
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C;Accession: G86403

Chin, C.W.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huzar, L.

Asture 408, 816-820, 2000

A,Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A,Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Wu, D.; Yu, G.; Fraser, C.M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference number: A86141; MUID:21016719; PMID:11130712

A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C)Accession: B60950
R;Law, A.; Scott, J.
J. Lipid Res. 31, 1109-1120, 1990
A;Title: A cross species comparison of the apolipoprotein B domain that binds to the A;Reference number: A60950; MUID:90324804; PMID:2373961
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A,Residues: 1-289 <STO>
A,Fross-references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141
C,Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Rattus norvegicus (Norway rat)
C.Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3% hypothetical protein F28L5.13 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                    Gaps
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                                                                                                     Length 4568;
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                                                                                               Score 41; DB 2; Length 456
Pred. No. 1.8e+02;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
F;2202-2209/{
m Region}: nucleotide-binding motif A (P-loop) F;2530-2537/{
m Region}: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56.3%; Score 40; DB 2;
66.7%; Pred. No. 15;
1ive 2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  apolipoprotein B-100 - rat (fragment)
                                                                                               57.7%;
41.7%;
                                                                                                                                                           Conservative
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1852 CFQWQSQLRYIQ 1863
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Best Local Similarity
6; Conserve
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7, Conserva
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                                                                                        Query Match
Best Local Similarity
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, RESULT 12

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A;Note: this allele is designated A*3401 (formerly HLA-Aw34.1)

R;Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour,
submitted to the EMBL Data Library, August 1991
A;Description: Molecular definition of HLA-A,B antigens of black populations: Implicatio
A;Reference number: S16766
A;Resesion: S16771
A;Molecule type: mRNA
A;Residues: 1-2, V', 4-89, N', 91-120, 'I', 122-128,'S', 130-137,'R', 139-179,'L', 181-248,'I',
A;Coss-references: EMBL:X61705
A;Note: this allele is designated A*3402
C;Genetics:
A;Gene: GDB:HLA-A
A;Cross-references: GDB:119310; OMIM:142800
C;Genetics:
A;Genetics: A;Genetics: GDB:119310; OMIM:142800
C;Genetics: A;Genetics: EMBL:X61704
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: heterodimer; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>F;220-285/Domain: immunoglobulin homology <NMM>
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Gaps · 0 54.9%; Score 39; DB 2; Length 365; Conservative 2; Mismatches 1; Indels Query Match Best Local Similarity Best Loca Matches

·:

4 WERNMRKVR 12

84 WDRNTRKVK 92 d

RESULT 15

Outer capsid protein VP4 - human rotavirus B
C;Species: human rotavirus B
C;Species: human rotavirus B
C;Species: human rotavirus B
C;Accession: A45687
C;Accession: A45687
C;Accession: A5887
C;Accession: A78887
C;Accession: A788887
A;Accession: A78887
A;Accession: A788887
A;Accession: A78887
A;Accession: A788887
A;Accession: A78887
A;Accessio

A, Accession: A45687

A;Status: preliminary
A;Molecule type: nucleic acid
A;Moscile expense inconsistent with the nucleotide translation
A;Note: sequence inconsistent with the nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:130353, NCBIP:130355)
C;Superfamily: rotavirus core protein

Gaps Query Match
54.9%; Score 39; DB 2; Length 749;
Best Local Similarity 50.0%; Pred. No. 65;
Matches 6; Conservative 1; Mismatches 5; Indels

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1 CFQWERNMRKVR 12

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195 CFTWDMNCANVR 206

Search completed: February 21, 2003, 07:47:56 Job time : 10.65 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2003, 07:25:55 ; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-84 71 1 CFQWERNMRKVR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cion	homo sapien		•н		mus musculu	chlamydomon	caenorhabdi	homo sapien	rotavirus (liberibacte	drosophila	arabidopsis	thermoanaer	methanococc	mus musculu	rattus norv	homo sapien	caenorhabdi	arabidopsis	canis famil	rattus norv	mus musculu	propionibac	gallus gall	cricetulus	homo sapien	mesocricetu	mus musculu	rattus norv	Borghum bic	rhizobium s	simian immu	homo sapien
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SUMMARIES		TAN	IDR	IH	SE	ISE	RE	EL	IAN	Ą	JAF.	E	哥	N.I.	J.A	SE		IAN	EL	HI	A		SE	FR	¥	œ	z	ı.	· ·		BI	SN	4	z
SUMMZ	А	TRFL HUMAN	TRFL CAMDR	TRFL CAPHI	TRFL_HORSE	TRFL_MOUSE				VP4_ROTGA				RL28_THETN	YE83 METUA	CATL_MOUSE	CATL_RAT	YOOR HUMAN		ATX1 ARATH	DMD CANFA	CATK_RAT	CATJ MOUSE	MUTA PROFR	EF2_CHICK	EF2_CRIGR	EF2_HUMAN	EF2 MESAU	EF2 MOUSE		- 1	Y4LN RHISN	VIF SIVS4	SH4_HUMAN
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*	Query Match	95.		-		59.5			54.9														50.7						50.7				σ.	
	Score	9	51	51	43	42	41	40	б	50 1	ж С	38	38	37	3.7	37	37	37	37	37	37	36	36	910	3 6	36	36	36	36	36	36	32	35	32
	Result No.	1	7	m	4	ın '	9	7	Φ (ን (7.0	77.	12	13	14	15	16	17	18	19	20	27	22	570	470	25	970	7.7	28	29	30	31	35	33

Q13515 homo sapien Q9pjj9 chlamydia m Q9ulc6 homo sapien O67763 aquifex aeo Q9x6y2 aquifex aeo Q9vm75 drosophila P23374 bacillus st P01432 naja mossam Q92aj2 listeria mo	Q99up4 staphylococ Q55185 synechocyst P53661 mycoplasma
BFS2 HUMAN SYH CHLMU PD11 HUMAN RPOC AQUME RPOC AQUME RPOC AQUMP BP28 DROME RL28 BACST NXS3 NAJMO RLS8 LISMO	RL28_STAAM Y495_SYNY3 Y125_MYCCA
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415 428 663 1574 1576 2096 60 62	62 246 267
44444444 999999777 6669999777	47.9 47.9 6.74
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8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	4 4 4 5 4 5

ALIGNMENTS

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us-09-743-107b-84.rsp

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12-MAR-97.
21-APR-97.
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1LCT; 31-OCT-93.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-96.
                                                                                                                                                                                                                                                 PubMed=9873069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X52941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S11228;
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1LFG;
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1LGB;
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      SEQUENCE OF 237-711 FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansaria R., Schutz R.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U.,
Sagripanti J.L.;
                                                                                                                                                                                                                              "The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-90064528; PubMed-2585506; Anderson B.F., Baker B.N.; Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker B.N.; Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
                                                                                                                                                                                            MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                     MEDLINE=82262043; PubMed=7049727;
Meiz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Mutagenesis of the histidine ligand in human lactoferrin: iron binding properties and crystal structure of the histidine-
                                                                                                                                                                                                                                                                                                                                                                                                                Rado T.A., Wei X., Benz B.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library an
expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                 SEQUENCE OF 20-711.

MEDIANE=85076667; PubMed=6510420;
MELZ-Boutigue M.-H., JOlles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
                                                                                                                                                                                  PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haridas M., Anderson B.F., Baker B.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                              Jolles P.; ""An 88 amino acid long C-terminal sequence of human
                                  Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353.
                                                                                                                                                                                                                                                                   Biochim. Biophys. Acta 670:243-254(1981)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; Pubmed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
                                                             Nucleic Acids Res. 18:4013-4013(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Acta Crystallogr. D 51:629-646(1995)
                                                                                                                                                           J. Biochem. 145:659-666(1984)
                         MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88001031; PubMed=3477300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97156796; PubMed=9003186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Mol. Biol. 209:711-734 (1989).
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                                                                                                                                                                                                                                                                                                                                                                  FBS Lett. 142:107-110(1982).
                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 436-711 FROM N.A.
  OF 3-711 FROM N.A.
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            IISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                           SEQUENCE OF 609-711
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RM SIN X.L., Baker H.M., Shary S.C., Jameson G.B., Baker B.N.; Reversellust of recombinant human lactoferrin expressed in Aspergillus Acts after (1988).

Acts after (1988).

Acts after (1988).

RM STATE (1989).

RM STATE (1989).
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Capra hircus (Goat).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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. .) (POTENTIAL).
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G -> A (IN REF. 2).
G -> A (IN REF. 2).
LLS -> PLF (IN REF. 2).
L -> F (IN REF. 2).
A -> P (IN REF. 2).
A -> P (IN REF. 2).
A -> Q (IN REF. 2).
A -> Q (IN REF. 2).
A -> Q (IN REF. 2).
W, OBOCLT5AOB69D430 CRC64;
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                   IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 1 (BY SIMILARITY)
IRON 2 (BY SIMILARITY)
ANION (BY SIMILARITY)
ANION (BY SIMILARITY)
N-LINKED (GLCNAC. )
N-LINKED (GLCNAC. )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRFL CAPHI STANDARD, (29479, 1029479, 029477, 029479, 15-DEC-1998 (Rel. 37, Last sequence update) 15-UBC-1998 (Rel. 41, Last amnotation update) 15-UDM-2002 (Rel. 41, Last amnotation update)
BY SIMILARITY.
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MEDLINE=94380047; PubMed=8093048;
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708 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                            Camelus dromedarius (Dromedary) (Arabian camel).
Sukaryota: Metazoa; Chordata; Craniata; Vortebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
NCBI_TaxID=9838;
                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
                                            .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; 077811; 1B1X.
InterPro; IRP001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
          Length 711;
 ch 95.8%; Score 68; DB 1; Length 711
l Similarity 91.7%; Pred. No. 0.00026;
11; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                     TRFL_CAMDR STANDARD; PRT; 708 AA. 09TUM0; 09MCS5; 16-0CT-2001 (Rel. 40, Last sequence update) 15-0CT-2001 (Rel. 40, Last sequence update) 15-UW-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN
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363
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 Query Match
Best Local Similarity
Matches 11; Conserv
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Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                  Būkaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                               15-UTL-1999 (Rel. 38, Created)
15-UTL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB=Milk;
MEDLINE=99296631; PubMed=10365507;
                                                                                                                                                                                                                                                                                          Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9796;
                                                                                                                   TRFL HORSE
077811;
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                                                                    RESULT 4
                                                                                                                                          HERETEREE TERETEREE BREEF BREE
                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
                                                                                                                                                                                                                                                                                                                       HSSP, 077698; ICEZ.
InterPro: IPR001156; Transferrin.
Pfam; PF00405; transferrin, 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
TRANSFERRIN. 3; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
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IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
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(GLCNAC. .)
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DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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2 -> K (IN REF. 2).
5 -> K (IN REF. 2).
5 -> P (IN REF. 2).
5 -> G (IN REF. 2).
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                                                                                                                                                                                                                                                                        EMBL; U53857; AAA97958.1; -.
EMBL; X78902; CAA55517.1; -.
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Best Local Similarity 63.v.,
7; Conservative
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resolution...;
J. Mol. Biol. 289.303-317(1999).

-!-FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
-!-SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAINS: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R EMBL, AJ0100930, CAA09407.1; -.
R PDB, 1B1X; 02-DEC-99.
R PDB, 1B7Z; 02-FEB-99.
R PDB, 1B7Z; 02-FEB-99.
R PDB, 1B7Z; 02-FEB-99.
R PDB, 1B7Z; 02-FEB-99.
R PRINTS; PR00402; TRANSFERIN.
R PRINTS; PR000094; TR FER; 2.
R PROSITE; PS00206; TRANSFERIN 1; 2.
R PROSITE; PS00207; TRANSFERIN 2; 2.
R PROSITE; PS00207; TRANSFERIN 3; 1.
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1; Indels

3; Mismatches

CFQWERNMRKV 11 38 CYQWQRRMRKL 48

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Best Local Similarity 54.5
Matches 6; Conservative
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"Characterization of estrogen-responsive mouse lactoferrin promoter.";
J. Biol. Chem. 266:21880-21885(1991).
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                   Gaps
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Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                         (GLCNAC. ..) (FOLENTIAL).
                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                   ..
0
                                                                                                                                                                60.6%; Score 43; DB 1; Length 695;
                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                  07BB84D50E1B165D CRC64;
                                               IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                          N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                 TRFL_MOUSE STANDARD; PRT; 707 AA. P08071; P70690; Q61799; Q922P2; C1-AUG-1988 (Rel. 08, Created) C1-AUG-2002 (Rel. 41, Last sequence update) C15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                         Pred. No. 5.4;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Biol. Chem. 262:10134-10139(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-14 FROM N.A. MEDLINE=92042099; PubMed=1939212;
                                                                                                                                                  75991 MW;
                                                                                                                                                                         58.3%;
                                                                                                                                                                                 Conservative
                                              66
98
1198
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                                                                                                                                                                                              CFQWERNMRKVR 12
                                                                                                                  469
143
187
287
482
695 AA;
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                                                                                                                                                                        Local Similarity
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TISSUE=Uterus;
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44463
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6531
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667
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7399
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ANION (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

MR -> LQG (IN REF. 1).

R -> Q (IN REF. 2).

M -> L (IN REF. 2).

S -> T (IN REF. 2).

L -> U (IN REF. 1).

A -> D (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001156; Transferrin.
Prim; Pr00405; transferrin; 2.
PRIMITS; PR00402; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSTIE; PS00205; TRANSFERRIN 1; 1.
PROSTIE; PS00205; TRANSFERRIN 2; 2.
PROSTIE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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2; Mismatches
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                                                                                                                                                                                                                       EMBL; J03298; AAA40525.1; -.
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Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.

15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Hypothetical protein F30B5.4 in chromosome IV

Caenorhabditis elegans.

F30B5.4

STRAIN=Bristol N2; Miller N., Bradshaw H.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.

SEQUENCE FROM N.A. NCBI_TaxID=6239;

Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

Waterston R.;

REVISIONS

Tue Dec

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                                                                                                                                                                                                                                                                                   J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                             Mitchell D.R., Brown K.S., "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                              DYNEIN HAS ATPASE ACTIVITY.
-!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                           Chlamydomonas reinhardtii.
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COLLED COLL (POTENTIAL).
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InterPro; IPR004273, Dynein heavy.
Pfam; PF03028; Dynein heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella; Coiled coil.
DOMAIN 277 293 COILED COIL (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
9A9A5393C7C36AE7 CRC64;
                                                                        Last sequence update)
                               PRT; 4568 AA
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                                                                                                    flagellar outer arm,
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                                                                                                                                                          Chlamydomonadaceae; Chlamydomonas
                                                                                                                                                                                                                              MEDLINE=94274778; PubMed=8006077;
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                                                         (Rel. 35, Created)
(Rel. 35, Last seg
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                              STANDARD;
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2202 220
2530 253
2879 288
4568 AA;
                                                                                                 Dynein beta chain,
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3339
3648
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                                                       01-NOV-1997
01-NOV-1997
                            DYHB_CHLRE
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56.3%; Score 40; DB 1; Length 455; 60.0%; Pred. No. 12;

Best Local Similarity

Query Match

Hypothetical protein. SEQUENCE 455 AA; 51148 MW; D8E6909408FD6C69 CRC64;

EMBL; U42437; AAA83493.2; -. WormPep; F30B5.4; CE28552.

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     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=9235211; PubMed=8475492;
Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit E.D., Parham P.;
"Structural diversity in the HLA-Al0 family of alleles: correlations
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
"Distinctive HLA-A,B antigens of black populations formed by
interallelic conversion.";
                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                      P30455; P30454;
01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34(A-10) alpha chain
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0
   3; Indels
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1; Mismatches
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SEQUENCE FROM N.A. (A*3401/A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Immunol. 149:3411-3415(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Antigens 41:72-80(1993)
 6; Conservative
                                                                                                                                             STANDARD;
                                                                102 CIQWELNRRR 111
                                1 CFOWERNMRK 10
                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       with serology.";
                                                                                                                                                                                                                                                          HLA-A OR HLAA.
                                                                                                                                             1A34 HUMAN
                                                                                                             RESULT 8
1A34_HUMAN
Matches
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Gaps

0;

3; Indels

4; Mismatches

80;

Pred.

41.7%;

5; Conservative

Matches

1852 CFQWQSQLRYIQ 1863

1 CFQWERNMRKVR 12

455 AA.

PRT;

RESULT 7
YKYL CABEL
1D YKYL CABEL STANDARD;
1AC Q19910;
DT 16-OCT-2001 (Rel. 40, Created)

Mackow E.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M., "Identification and baculovirus expression of the VP4 protein of the

SEQUENCE FROM N.A. MEDLINE=93233240; PubMed=8386274;

NCBL_TaxID=12705;

01-JUN-1994 (Rel. 29, Last sequence update) 01-JUN-1994 (Rel. 29, Last annotation update) Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).

Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus). Viruses, dsRNA viruses, Reoviridae, Rotavirus.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                        HLA CLASS I HISTOCOMPATIBILITY ANTIGEN,
                                                   POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO
                IMMUNE SYSTEM.
JNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 39; DB 1; Length 365;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  063BF63E6E6E01F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AW-34 (A-10) ALPHA CHAIN.
EXTRACELLULAR ALPHA-1.
EXTRACELLULAR ALPHA-2.
EXTRACELLULAR ALPHA-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 I -> V (IN A*3402).

FTIG=VAR 004390.

R -> N (IN A*4402).

FTIG=VAR 004380.

R -> I (IN A*3402).

FTIG=VAR 004381.

P -> S (IN A*3402).

FTIG=VAR 004382.

/ FTIG=VAR 004382.

S -> R (IN A*3402).

FTIG=VAR 004383.

W -> L (IN A*3402).

FTIG=VAR 004383.

W -> L (IN A*3402).

FTIG=VAR 004383.

I -> I (IN A*3402).

I -> I (IN A*3402).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC TAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          004385
                                                                                                                                                                                                                                                                                                                          Pfan, PF00047; ig; 1.
Ftan; PF00129; MHC 1; 1.
ProDom; PF00050; MHC 1; 1.
SMART; SM00407; IGG1; 1.
PROSITE; PS00290; IG MHC; 1.
MHC 1; Transmembrane; GlycoprosiGIGNAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 AA; 41055 MW;
                                                                                                                                                                                                         EMBL; X61704; CAA43873.1; -.
                                                                                                                                                                                                                                                                                  InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR001039; MHC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%;
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332
332
345
1110
1288
283
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                                                                                                                                                                                                                                    PIR; S16767; S16767.
PIR; S16771; S16771.
HSSP; O19673; 1HSB.
MIM; 142800; -.
                                    MICROGLOBULIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          312
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                                                                             A*3401
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DOMAIN
DOMAIN
TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Planet P., Jagoueix S., Bove J.M., Garnier M.,
"Detection and characterization of the African Citrus Greening
Liberobacter by amplification, cloning and sequencing of the rplKAJL-
TPOBC Operon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB.1995 (Rel. 31, Created)
1-FEB.1995 (Rel. 32, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (EC 2.7.7.6) (Transcriptase beta chain) (RA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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Bacteria, Profeobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae, Candidatus Liberibacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
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0
                                                                                                                                                                                                                                                                                                                  human group B rotavirus ADRV.",
J. Virol. 67:2730-2738(1993).
-!- SUBCELLULAR LOCATION: Outer capsid.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54.9%; Score 39; DB 1; Length 749; 50.0%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. . .) (PO D1223527DEAE0F21 CRC64;
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1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED
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InterPro, IPR000416, Cap VP4.
Pfam; PF00426, VP4, 1.
Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          195 CFTWDMNCANVR 206
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749 AA;
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620
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Best Local
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SOURCE STATE STATE
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Gaps

ö;

2; Mismatches

6; Conservative

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Best Local Similarity

Matches

749 AA.

VP4 ROTGA STANDARD; 004916; 01-JUN-1994 (Rel. 29, Created)

RESULT 9 VP4 ROTGA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holf R.A., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
An K.H., Doyle C., Baxerer B.G., Helt G., Welson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Frannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Bernan B.P., Bhandari D., Bolshakov S.,
Burtis K.C., Busam D.A., Buller H., Cadieu E., Center P., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dignar-Rocha S., Pleischmann W.,
A Durbin K.J., Evangelista C.C., Ferriaz C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Mandibulata, Pancrustacea, Hexapoda,
Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera;
Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                       {RNA}(N).
-!- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                          CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McCormick A.V., Goldberg M.L.; "Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                  SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                                     53.5%; Score 38; DB 1; Length 146; 60.0%; Pred. No. 8.1; ive 0; Mismatches 4; Indels
                                                                                                                                                                                                                                                                  Pfam, PF00562; RNA_pol_B; 1.7
PROSTIE; P801166; RNA_F0L_BETA; PARTIAL.
Transferage; Transcription; DNA-directed RNA polymerase.
NON_TER 146 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                         146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9XZL8; Q9V391;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            292 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                      InterPro; IPR001572; RNA_pol_B.
                                                                                                                                                                                                                                                                                                                                                                  60.0%;
                                                                                                                                                                                                                                      EMBL; U09675; AAA19557.1; -
                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWERNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                         10 CVQWSRGARK 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nebula protein.
                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLA DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       females
                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 11
NLA DROME
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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Heanan T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Linkel B.E., Kodira C.D., Kraft C., Karvitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., Mosherson D.,
A Markulov G., Milahina N.V., Mobarry C., Morris J., Mosherfi A.,
Nelson D.R., Nelson K., Nixon K., Nurshy D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Resee M.G.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
Ralazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Resee M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Syier B., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syier R., Spradling A.C., Stapleton M., Strong R., Sun E.,
Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Globs R.A., Myers E.W., Rubin G.M., Venter B., Wang A.H.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
R. The genomes sequence of Drosophila melanogaster.",
R. Science 287:2185-2195-2195-2000).
C. -- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE.
C. -- SIMILARITY: BELONGS TO THE DSCRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseaisb-sib.ch).
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eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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MEDLINE-21016721; PubMed=11130714;
Tabata S., Kaneko T., Nakamura Y., Kotani H., Kato T., Asamizu E.,
Tabata S., Kaneko T., Nakamura Y., Hosouchi T., Kawashima K.,
Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakayama S.,
Nakazaki N., Naruo K., Okumura S., Shinpo S., Takeuchi C., Wada T.,
Watanabe A., Yamada M., Yasuda M., Sato S., de la Bastide M.,
Huang E., Spiegel L., Gnoj L., O'Shaughnessy A., Preston R.,
Habermann K., Murray J., Johnson D., Rohlfing T., Nelson J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31423 MW; 64FlbbF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C911 ARATH STANDARD; PRT; 502 AA. Q9FG65; O65789; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Cytochrome P450 91A1 (EC 1.14...).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
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EMBL; AE003712; AAF55285.1; -.
FlyBase; FBgn0026629; nla.
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SEQUENCE
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Stoneking T., Pepin K., Spieth J., Sekhon M., Armstrong J., Becker M., Belter E., Cordum H., Cordes M., Courtney L., Courtney W., Dante M., Du H., Edwards J., Fryman J., Haakensen B., Lamar E., Latreille P., Leonards J., Meyer R., Mulvaney E., Ozersky P., Riley A., Strowmatt C., Ra Wagner-McPherson C., Wollam A., Yoakum M., Bell M., Dedhia N., Rairchoff K., Rodriguez M., Hoon See L., Vil D., Baker J., Rirchoff K., Toth K., King L., Bahret A., Miller B., Marra M., Ra Martienssen R., McCombie W. R., Wilson R.K., Murphy G., Bancroft I., Ra Volckart G., Wambutt R., Duesterhoeft A., Siekema W., Pohl T., RA Langham S.-A., McCullagh B., Robben J., Grymonprez B., Zhmmermann W., Ramsperger U., Medler H., Balke K., Wedler E., Peters S., Hempel S., Weitzenegger U., Mothe G., Rose M., Hauf J., Berneiser S., Hempel S., Weitzenegger T., Bothe G., Rose M., Hauf J., Berneiser S., Hempel S., Reldpausch M., Lamberth S., Villarroel R., Gielen J., Ardiles W., Schueller C., Zaccaria P., Mewes H.-W., Bevan M., Fransz P.F.; Relfiana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the Buropean Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Oxidoreductase, Monooxygenase, Transmembrane, Heme, Multigene family.
TRANSMEM 6 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                            Mizutani M., Ward E., Ohta D.,
"Cytochrome P450 superfamily in Arabidopsis thaliana: isolation of
cDNAs, differential expression, and RFLP mapping of multiple
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                           cytochromes P450.";
Plant Mol. Biol. 37:39-52(1998)
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BINDING 440 440 HEME (BY SIMILARITY).
SEQUENCE 502 AA; 56723 MW; 1A348A8DD76A41BO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=cv. Columbia;
MEDLINE=98281573; PubMed=9620263;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB026661; BAB09361.1; -.
                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 3-502 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            50S ribosomal protein L28. RPMB OR TTE1495.
                                                                                                                                                                                                                                                                                                     Nature 408:823-826(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             460 CFEWER 465
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Q8R9Ū1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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STRAIN-JAL-1 / DSW 2661 / ATCC 43067;

STRAIN-JAL-1 / DSW 2661 / ATCC 43067;

BULL C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

Sutton G.G., Rikhuss B.F., Weinstock K.G., Merrick J.M., Glodek A.,

Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Utterbeack T.K., Kalley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,

Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
SEQUENCE FROM N.A.
STRAIN=MB4 / JCM 11007;
STRAIN=MB4 / JCM 11007;
STRAIN=MB4 / JCM 11007;
Bab Q., Tian Y. Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Xu Y., Liai X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T., tengcongensis genome.";
                                                                                                                                                                  Genome Res. 12:689-700[2002].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 37; DB 1; Length 62;
Pred. No. 5.1;
3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanocaldococcus.
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                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AE013107; AAM24713.1; -. Ribosomal protein; Complete proteome. SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-0cT-2001 (Rel. 40, Created)
16-0cT-2001 (Rel. 40, Last sequence update)
16-0cT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52.1%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein MJ1483,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=2190;
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Q58878;
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YE83 METUA
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Gaps
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-!- SUBUNIT: DIMER OF A HEAVY AND A LIGHT CHAIN LINKED BY DISULFIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87033683; PubMed=3533924; Portroy D.A., Exidexion A.H., Kochan J., Ravetch J.V., Unkeless J.C.; "Cloning and characterization of a mouse cysteine proteinase."; J. Biol. Chem. 261:14697-14703(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN 1988 (Rel. 06, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Joseph L.J., Chang L.C., Stamenkovich D., Sukhatme V.P., "Complete nucleotide and deduced amino acid sequences of human and murine preprocathepsin L. An abundant transcript induced by transformation of fibroblasts."

J. Clin. Invest. 81:1621-1629(1988).
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MEDLINE-86271744; PubMed=3755373;

Denhardt D.T., Hamilton R.T., Parfett C.L.J., Edwards D.R.,
Pierre R.S., Waterhouse P., Nilson-Hamilton M.;

"Close relationship of the major excreted protein of transformed
murine fibroblasts to thiol-dependent cathepsins.";

Cancer Res. 46:4590-4593(1986)

-! FUNCTION: IMPORTANT FOR THE OVERALL DEGRADATION OF PROTEINS IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Stearns N.A., Dong J., Pan J.X., Brenner D.A., Sahagian G.G., "Comparison of cathepsin L synthesized by normal and transformed cells at the gene, message, protein, and oligosaccharide levels."; Arch. Biochem. Biophys. 283:447-457(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                          ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=88076849; PubMed=3689328;
Troon B.R., Gal S., Gottesman M.M.,
"Sequence and expression of the cDNA for MEP (major excreted protein), a transformation-regulated secreted cathepsin.";
Biochem. J. 246:731-735(1987).
                                                                 52.1%; Score 37; DB 1; Length 152; 50.0%; Pred. No. 13;
                                                                                                                                      3; Indels
152 AA; 17659 MW; 90227132448E8802 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND CARBOHYDRATE-LINKAGE SITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBCELLULAR LOCATION: LyBOSOMA1.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.
                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=88213715; PubMed=2835398;
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SEQUENCE OF 89-300 FROM N.A.
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                             Local Similarity
nes 5; Conserv
                                                                                                                                                                                             2 FOWERNMRKV 11
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P06797;
SEQUENCE
                                                              Query Match
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CATL MOUSE
TO POST MOUSE
TO 10-10AN
DT 01-10AN
DE CATLE PO
CASTLE PO

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                        InterPro; IPR000668; Peptidase C1.
InterPro; IPR000169; SHprot_acsite.
Pram; Pr00112; Peptidase C1; 1.
Pr001012; Peptidase C1; 1.
Pr000m; P0000158; Peptidase C1; 1.
PROSTIE; PS00139; THIOL_PROTEASE_CVS; 1.
PROSTIE; PS00640; THIOL_PROTEASE_HIS; 1.
PROSTIE; PS00640; THIOL_PROTEASE_ASN; 1.
Hydrolase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
PROPEP 11 17 ACTIVATION PEPTIDE.
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CATHEPSIN L, LIGHT CHAIN.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
BY SIMILARITY.
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M -> I (IN REF. 2).
G -> R (IN REF. 3).
FE6747043307AD98 CRC64;
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                                                                                                                    EMBL; X06086; CAA29470.1; -.
EMBL; J02583; AAA37445.1; -.
EMBL; M20495; AAA39984.1; -.
EMBL; X04392; CAA27980.1; -.
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55.6%;
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PIR; S13890; S13890.
                                                                                                                                                                                                                                            MGD; MGI:88564; Ctsl
                                                                                                                                                                                                               1CJL.
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MEROPS; C01.032;
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Q91zd5 mus musculu
Q91z75 mus musculu
Q31215 mus musculu
O19441 mus musculu
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O31090 rhizobium 1
Q96m21 homo sapien
Q8r224 mus musculu
Q92kp4 helicobacte
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Q9hpa3 halobacteri
Q98x85 arabidopsis
Q19153 caenorhabdi
Q8r9u1 thermoanaer
    09xhp1 sesamum ind 08yp77 anabaena sp 09daz8 mus musculu
                                                                                                                                                                                                                                                                                 Q9szt6 arabidopsis
023154 arabidopsis
Q9lhal arabidopsis
Q8s487 zea mays (m
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O92283 molluscum c
O77855 human immun
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023155 arabidopsis
09szt6 arabidopsis
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09yqc0 human immun
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ol-MAY-2000 (TERMBLrel. 13, Created)
Ol-MAY-2000 (TERMBLrel. 13, Last sequence update)
Ol-MAY-2000 (TERMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa, Chordata; Craniata, Vertebrata; Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC022347; AAH22347.1; -. SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TCD2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  711 AA.
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Q9SW68
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Q9SX85
    Q9XHP1
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   PRELIMINARY;
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   SEQUENCE FROM N.A.
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Q77856 human immun
Q99910 human immun
Q9c6n2 arabidopsis
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09xfd5 oryza sativ
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Q8tax2 homo sapien
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Q9ucy5 homo sapien
Q9tr80 ovis aries
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Ogsrr2 guillardia
Og3780 caenorhabdi
                                                                                    2003, 07:25:55 ; Search time 20.8 Seconds (without alignments) 118.873 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
 GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                         , 671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries.
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                                                      OM protein - protein search, using sw model
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Q9UCY5
Q9TR80
Q8Z462
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sp_mammal:*
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sp_phage:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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Match Length
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Result

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Gaps

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Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
                                                                                                                                                                            "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-GMIN00;

MEDLIKE-21661879; PubMed=11823852;
Salanoubat M., Genin S., Artigueneve F., Gouzy J., Mangenot S.,
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                         62.0%; Score 44; DB 16; Length 511; 58.3%; Pred. No. 7.5; ive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 43; DB 16; Length 279;
Pred. No. 6;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                          EMBL, ALC27276, CAD06049.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31541 MW; ABB38818004B2EDA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OBXEE2;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OSKEDS;
01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOV-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ralstonia solanacearum (Pseudomonas solanacearum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               279 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               105 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 415:497-502(2002).
EMBL; AL646079; CAD17685.1;
InterPro; IPR004843; M-ppestrase.
InterPro; IPR004844; S/T phosphtse.
Pfam; PF00149; Metallophos; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmid; Complete proteome
                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          350 CFAWDMNKAKVR 361
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244 CFQWEKGTRTAK 255
                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid megaplasmid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=305;
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                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8XSE2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          O9XFD5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8XSE2
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MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                 Sato I.;
"Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                          Score 59; DB 4; Length 38;
Pred. No. 0.00085;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.6%; Score 48; DB 6; Length 33; 54.5%; Pred. No. 0.076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                      Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP; 077699; 1CE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical protein STY3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                            seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; IBKA.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                  SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
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                                                                                                                                                                                                                                                                                                                          83.1%;
90.9%;
                                                                                                                                                                                                                                                                                                                                                                       10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mammalia, Eutheria, Cetar
Bovidae, Caprinae, Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                2 FOWERNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            21 FQWQRNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWERNMRKV 11
                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep)
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                            NCBI_TaxID=9606;
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Matches
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Gaps

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TISSUE=PLACENTA,

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Isogai T., Ota T., Hayashi K., Shiratori A., Sudo H.,

Magatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,

Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,

Wamamoto J., Wakamatau A., Nakamura Y., Nagahari K., Masuho Y.,

Ninomiya K., Iwayanagi T.,

Ninomiya K., Iwayanagi T.,

Ninomiya K., Iwayanagi T.,

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                       59.2%; Score 42; DB 4; Length 466; 66.7%; Pred. No. 16; cive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                          PROSITE; PS00499; C2 DOMAIN 1; UNKNOWN 1.
PROSITE; PS50004; C2 DOMAIN 2; 1.
PROSITE; PS00030; RRM RNP 1; UNKNOWN 1.
SEQUENCE 466 AA; 53192 MW; E4113A5062F58D6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 AA
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                                                                                                                                                                                                     EMBL, AK002037; BAA92048.1; -... HSSP; P21707; 1BYN.
InterPro; IPR000008; C2.
InterPro; IPR000504; RNA_rec_mot.
Pfam; PP00168; C3; 1.
PRINTS; PR00360; C2DOMAIN.
SWART; SM02339; C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Guillardia theta (Cryptomonas phi).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00141; PROTEASOME.
                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 CFQWESTLR 277
                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWERNMR 9
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Q93780
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Oryza sativa (Rice).
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoideae, Oryzeae, Oryza.
                                                                                                                   Liu J., Yang J.;

Liu J., Yang J.;

"Suppression subtractive hybridization (SSH) identified candidate genes that are differentially expressed at rice young panicle.";

Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL, AR140486; AAD29659.1;

InterPro; IPRO01128; Cytochrome_P450.

Pfam; PF00067; p450; ...
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Mammalia, Butheria, Frimates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0TJ-2002 (TrEMBLrel. 21, Last annotation update)
CDNA FLJ1175 fis, clone PLACE1007375, weakly similar to phorbol
ester/diacylglycerol-binding protein UNC-13.
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                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO25708; AAH25708.1; -..
Hypotherical protein.
SEGUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
                                                                                                                                                                                                                                                                                               SEQUENCE 105 AA; 11912 MW; BOEEFCDD487E19F9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08TAX2;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ11175.
                                                                                                                                                                                                                                       PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1. Heme; Monooxygenase; Oxidoreductase.
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                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 70.0%
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les 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                        SEQUENCE FROM N.A.
TISSUE=PANICLE;
                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWERNMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                     61 CPOWERLGKK 70
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                                                               NCBI_TaxID=4530;
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Q9NUS2
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MEDLINE=21223349; PubMed=11323671;
Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.T., Wu X., Reith M., Cavalier-Smith T., Maier U.G.;
"The highly reduced genome of an englaved algal nucleus.";
Nature 410:1091-1096(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AA; 22691 MW; D30F5289CBC85049 CRC64;
                                                                                                                                                               Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia
NCBI_TaxID=55529;
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275 AA

PRELIMINARY;

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NCBI_TaxID=3702;
                                                            01-JAN-1998
01-MAY-1999
                                                                                                                                                                                                                                                                                                                            Query Match
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                                                    023230;
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                                        023230
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                   RESULT 12
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STRAIN=CV. STELLA D'ORO; TISSUE=SENESCING PETALS;
MEDLINE=99339248; Pubmed=1041293;
Panavas T., Pikula A., Raid D.D., Rubinstein B., Walker E.L.;
"Identification of senescence-associated genes from daylily petals.";
Plant Mol. Biol. 40:237-248(1999).
-- SIMILARIY: BELONGS TO THE CYTOCHROME P450 FAMILY.
BREL; AR082028; AAC34853.1; --
InterPro; IPR001128; Cytochrome_P450.
                                                                                       Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hemerocallis hybrid cultivar.
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Asparagales,
Hemerocallidaceae, Hemerocallis.
                                                                                                                                                                                                                                                                                                             ,
0
                                                                                                                                                                                                             "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998).
EMBL, Z81089; CAB03137.1; -. SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                  57.7%; Score 41; DB 5; Length 275; 63.6%; Pred. No. 14; 2; Indels ative 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 71.4%; Score 41; DB 10; Length 372; Similarity 71.4%; Pred. No. 19; 5; Conservative 2; Mismatches 0; Indels
                                                                                                                                                  Dobson K.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 372 AA; 41909 MW; 55FB3EAF9699595E CRC64;
                                  Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Senescence-associated protein 3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00385; P450.
PROSTIE; PS00086; CYTOCHROME P450; UNKNOWN 1.
Heme; Monooxygenase; Oxidoreductase.
NON TER
                                                                                                                                                                                                                                                                                                                                                                                                             372 AA.
                       Created)
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                                                                                                                                                                                           MEDLINE=99069613; PubMed=9851916;
       093786;
01-FEB-1997 (TrEMBLrel. 02, Cr
01-AUG-1998 (TrEMBLrel. 07, La
01-DEC-2001 (TrEMBLrel. 19, La
F53H4.4 protein.
                                                                                                                                                                                                                                                                                             Local Similarity 63.6
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                                                                            Caenorhabditis elegans.
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262 FQWKISMRKTR 272
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                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                              NCBI TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=80862;
                                                                                                                                               Dobson R
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Matches
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                                                                        01-MAY-1999 (TEMBLE-1. 10, Last sequence update)
01-UN-2001 (TEMBLE-1. 17, Last annotation update)
Trichohyalin like protein.
C7A10.840 OR AT4G36520.
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Aspnolitophyta; eudicotyledons; core eudicots; Rosidae; eurogids II; Brassicales; Brassicaceae; Arabidopsis.
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NCBI_TaxID=5691;
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Bevan M., Terryn N., Vos P., Heijnen L., Mewes H.W., Schueller C.,
Chalwatzis N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S., Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D., Gerrard C., Rajandream M.A., Barrell B.G.; Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases. EMBL; ALSS9782, CAB95377.1; -- EMBL/GenBank/DDBJ databases. InterPro, IPR002035; VWF.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.7%; Score 41; DB 10; Length 1432;
54.5%; Pred. No. 79;
ive 3; Mismatches 2; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; 299708; CAB16641.1; -
EMBL; ALIG1589; CAB80318.1; -
SEQUENCE 1432 AA; 163973 MW; 96CE6FECB9BF0538 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2186 AA; 245737 MW; 78BB75505012005A CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Conserved hypothetical protein CHRI.67.
     PRT; 1432 AA
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                                                            Created)
                                                      (TrEMBLrel. 05,
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Matches 6; Conservative
PRELIMINARY;
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Matches 5; Conservative
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RESULT 14

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Gaps

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Matches

01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) 01-DEC-2001 (TremBlrel. 19, Last annotation update) 01-DEC-2001 (Fragment).

91 AA.

PRT;

PRELIMINARY;

077856

977856

Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;

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PRT;
                 Envelope glycoprotein (Fragment).
PRELIMINARY;
                                       SEQUENCE FROM N.A.
                                          STRAIN=VTRJ07;
                                                                                  SEQUENCE
                                                                                         Query Match
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0909L0
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Tanuri A., Machado E., Caride E., Costa L.J., Telles J.G.,
"Primary infections with HIV-1 of women and their offspring in Rio de
Janeiro, Brazil: Finding of recombinant of HIV-1 subtypes B and F.";
Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AFI53457; AAFI6896.1;
InterPro; IPR000777; GPI20.
Pfam; PF00516; GPI20;
AMDS; Coat protein; Glycoprotein.
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115 AA; 12832 MW; 86E509D6F6978127 CRC64;
                                                                            Q9Q9L0;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                          Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBL_TaxID=11676;
                                                              115 AA.
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RESULT 15
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56.3%; Score 40; DB 15; Length 91; 60.0%; Pred. No. 6.5; 1; Indels tive 3; Mismatches 1; Indels

6; Conservative

Matches

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Query Match Best Local Similarity

NON TER NON TER SEQUENCE

91 AA; 10519 MW; EB20C63A22DA1288 CRC64;

MEDILINE-95191002; PubMed=7884875; Milken C.L., Dekker J.,
MEDILINE-95191002; PubMed=7884875; Milken C.L., Dekker J.,
Mulder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J.,
A Scherpbier H.J., de Perre P., Boer K., Goudsmit J.;
T. Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is
T. unrelated to time of HIV-1 RNA positivity in the child.";
I. Jirol. 69:2285-2296(1995).
R. EMBL, 247868; CAA87882.1; -.
R. InterPro; IPR00777; GP120.
R. Pfam; PF00516; GP120, 1.
M. AIDS; Coat procein; Glycoprotein.

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Search completed: February 21, 2003, 07:44:38 Job time : 21.8 secs
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Advanced glycosyla
Human lactoferrin
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Lactoferrin derive Lactoferrin derive Bovine lactoferrin Bovine lactoferrin Lactoferrin-derive Lactoferrin derive Lactoferrin-derive Lactoferrin-derive Anti-parasitic pep Thrombus formation

Lactoferrin-derive

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Human lactoferrin

Peptide for anti-u Human lactoferrin

Human lactoferrin

Human lactoferrin

OM protein

Run on:

Sequence:

Searched:

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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human lactoferrin derived peptide SEQ ID NO:85.
                                                                                                                                                                                                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                                                                                                                           AAR98553
AAR91852
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AAW14036
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AAR80263
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AAR21810
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98SE-0002562.
98SE-0004614.
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 WPI; 2000-147388/13.
WO200001730-A1.
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 AAY78085;
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| Sinbs2/gcgdata/geneseqg/geneseqg-embl/AA2001.DAT:*
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             GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Result No.

Matches Homo AAY78081 RESULT à 셤

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                     based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-incobial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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        New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 71; DB 21; Length 12; 100.0%; Pred. No. 2.4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                     AAY78001 to AAY78100 represent peptides having sequences
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                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY78081 standard; Peptide; 12 AA.
                                                          Claim 22; Page 36; 102pp; English
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98SE-0002562.
98SE-0004614.
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                          Sequence
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AAY78001 to AAY78100 represent peptides having sequences based on human

Claim 22; Page 36; 102pp; English.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             binding to specific lactoferrin receptors and are then transported through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collits, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also
lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infections and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                 94.4%; Score 67; DB 21; 91.7%; Pred. No. 0.00011;
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                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY78038 standard; Peptide; 12 AA.
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nes 11; Conserva
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29-DEC-1998;
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             Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                              Gaps
 fungicidal and bactericidal and may also be used as preservatives.
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98SE-0004614.
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29-DEC-1998;
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                                           Score 66; DB 21; Length 12;
Pred. No. 0.00016;
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                                             93.0%;
91.7%;
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Matches 11; Conserv
                                                            Local Similarity
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AAY78048 standard; Peptide; 13 AA.

(first entry)

25-APR-2000

AAY78048;

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such an infant and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                              AAY78037 standard; Peptide; 13 AA.
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1 CFQWQENMRKVR 12
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                                                                                                                                                                    AAY78037;
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AAY78001 to AAY78100 represent peptides having sequences based on human lattoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or prevention of the peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides he used an are also is the infant human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:49.
                                                                                                         Human lactoferrin derived peptide SEQ ID NO:48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 15; Page 74; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                    98SE-0002562.
98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB.
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29-DEC-1998;
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Gaps ò.

Best Local Similarity 91.7 Matches 11; Conservative

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RESULT 7 AAY78048

99WO-SE01230

06-JUL-1999;

13-JAN-2000

WO200001730-A1

Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lattoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fin food stuffs such as infant formula so be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would contain them to be used for the same purposes as lactoferrin at lower
                   Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; uninary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                          Baltzer L, Dolphin GT;
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                                                                                                                                                                                                                                                                                               98SE-0002562.
98SE-0004614.
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                                                                                                                                                               WO200001730-A1
                                                                                                               Homo sapiens.
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Gaps
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 Score 66; DB 21; Length 13;
Pred. No. 0.00018;
0; Mismatches 1; Indels
93.0%;
91.7%;
                         11; Conservative
             Local Similarity
                         Matches
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1 CFOWQENMRKVR 12 2 CPÓWORNMRKVR 13 ð

Human lactoferrin derived peptide SEQ ID NO:36. AAY78036 standard; Peptide, 14 AA. (first entry) 25-APR-2000 AAY78036; **AAY**78036

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; uninary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candia infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also an infant buman lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                       inflammations and tumors and for use in infant formula food
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Pred. No. 0.00019;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                        Dolphin GT
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                                                                                                                                                                                                                                        Baltzer L,
                                                                                                                                                                                                                                                                                                                                                       Claim 12; Page 69; 102pp; English.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as webrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
                                                                                                                                                              New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 66; DB 21; Length 14;
Pred. No. 0.00019;
); Mismatches 1; Indels
                                                                                                        Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:51.
                                                                                                      Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78051 standard; Peptide; 14 AA.
                                                                                                                                                                                                       Claim 15; Page 75; 102pp; English
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                                                                                                     Mattsby-Baltzer I,
            98SE-0002441.
98SE-0002562.
98SE-0004614.
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91.7%;
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                                                                         (ASCI-) A+ SCI INVEST AB.
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                 06-JUL-1998;
                                           29-DEC-1998;
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                               17-JUL-1998
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                                                                                                      Hanson LA,
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Gaps

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammantions and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and contains the costs.
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                                                          New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR98531-54 are peptides used in an anti-ulcer agent. The acin toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                                                                                                                                                                                                                                                                                                                                           93.0%; Score 66; DB 21; Length 14; 91.7%; Pred. No. 0.00019; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-ulcer agent; low toxicity; stable; heat-resistant.
Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - has low toxicity, is
Baltzer L,
                                                                                                      Claim 18; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR98554 standard; Peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-ulcer agent contg. peptide -
heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 11; 11pp; Japanese.
Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide for anti-ulcer agent.
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Best Local Similarity 91.7
Matches 11, Conservative
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                             WPI; 2000-147388/13
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AAY78062 standard; Peptide; 15 AA.

RESULT 14

AAY78062

25-APR-2000 (first entry)

AAY78062;

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                                                                                                                                                                                                                                                                                       Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                 Gaps
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Score 66; DB 17; Length 15;
Pred. No. 0.0002;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 66, DB 21; Length 15;
Pred. No. 0.0002;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dolphin GT;
                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Baltzer L,
                                                                                                                                                                    AAY78035 standard; Peptide; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 69; 102pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanson LA, Mattsby-Baltzer I,
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91.7%;
93.0%;
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                                                                                                                                                                                                                                (first entry)
                             11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ASCI-) A+ SCI INVEST AB.
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                                                           1 CFOWDENMRKVR 12
                                                                                        2 CFOWORNMRKVR 13
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                Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUL-1998;
                                                                                                                                                                                                                                25-APR-2000
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                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                             Matches
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4 CFÓWORNMRKVR 15

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides is preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                         Human, lactoferrin, modification, infection, inflammation, tumour,
food, infant formula, anti-inflammatory, anti-microbial, anti-tumour,
urinary tract infection, colitis, Candida infection, fungicidal,
bactericidal, preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
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                                                                                                        Human lactoferrin derived peptide SEQ ID NO:62.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 15; Page 81; 102pp; English.
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Best Local Similarity
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                                                                                                                                                                                                                                      sapiens.
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Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                          Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                            Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                         Claim 18; Page 81; 102pp; English.
                                                                                                                                                                               98SE-0002441.
98SE-0002562.
98SE-0004614.
          25-APR-2000 (first entry)
                                                                                                                                                                                                                       (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                           WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 15 AA;
                                                                                                                         WO200001730-A1.
                                                                                                                                                                               06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                              Homo sapiens.
                                                                                                                                                              06-JUL-1999;
                                                                                                                                            13-JAN-2000.
                                                                                                     Synthetic.
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99WO-SE01230.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through limiting to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bacterial and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower

. 93.0%; Score 66; DB 21; Length 15; 91.7%; Pred. No. 0.0002; tive 0; Mismatches 1; Indels 11; Conservative Best Local Similarity Query Match Matches

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Search completed: February 21, 2003, 07:37:15 Job time : 28.35 secs

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                                                                                                                                                                                                                                   US-08-204-487-3
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Sequence 1, Appli
Sequence 24, Appl
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                                                        February 21, 2003, 07:25:59; Search time 8.65 Seconds (without alignments) 40.818 Million cell updates/sec
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Sequence 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8,
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Sequence 3,
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Sequence 5,
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Sequence
Sequence
Sequence
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GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.*
                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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US-07-755-161A-10
                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
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US-08-381-984-24
US-08-381-984-25
US-09-508-734-4
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US-08-204-487-7
US-09-508-734-8
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US-08-406-271-5
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US-08-256-771-24
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                                                                                                                                                                        262574 seqs, 29422922 residues
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                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                       OM protein - protein search, using sw model
                                                                                                                                         BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                 US-09-743-107B-85
71
                                                                                                                     1 CFQWQENMRKVR 12
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Match Length DB
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                                                          Run on:
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28	99	93.0	54	~	US-08-464-182A-2	Sequence 2,	Appl
29	99	93.0	54	0	US-08-406-271-2	Sequence 2,	Appl
30	99	93.0	694	m	US-08-724-586-2	Sequence 2,	Appl
31	99	93.0	694	4	US-09-421-632-2	Sequence 2,	Appl
32	99	93.0	694	4	US-09-932-190-2	Sequence 2,	Appl
33	99	93.0	705	7	US-08-655-640-2	Sequence 2,	Appl
34	99	93.0	708	0	US-08-655-640-4	Sequence 4,	App1
35	99	93.0	711	Н	US-08-154-019-4	Sequence 4,	Appl
36	99	93.0	711	Н	US-08-461-333-4	Sequence 4,	Appl
37	99	93.0	711	m	US-08-464-167-4	Sequence 4,	Appl
38	99	93.0	711	m	US-09-158-313-4	Sequence 4,	Appl
33	99	93.0	711	4	US-08-476-798-4	Sequence 4,	Appl
40	63	88.7	711	Н	US-08-145-681-2		Appl
41	63	88.7	711	-1	US-08-250-308-2	Sequence 2,	Appl
42	63	88.7	711	Н	US-08-453-703-2	Sequence 2,	Appl
43	63	88.7	711	N	US-08-456-106-2	Sequence 2,	Appl
44	63	88.7	711	e	US-08-456-108-2	Sequence 2,	Appl
45	63	88.7	711	4	US-09-265-577-2	Seguence 2.	Appl

ALIGNMENTS

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HENGULT

US-08-204-487-3

US-08-204-487-3

Sequence 3, Application US/08204487

Sequence 3, Application US/08204487

Sequence 3, Application US/08204487

Sequence 3, Application US/08204187

PAPELICANT: NAKASHIMA, HIDERI
APPLICANT: NAKASHIMA, HIDERI
APPLICANT: NAKASHIMA, HIDERI
APPLICANT: TANAKA, SHIGBAKI
APPLICANT: TANAKA, SHIGBAKI
APPLICANT: UCHIDA, TOSHIAKI
TITLE OF INVENTION: UNIBILITYS
APPLICANT: UCHIDA, TOSHIAKI
TITLE OF INVENTION: UNIBILITYS

NUMBER OF SEQUENCES: 8

STATE: NOSTON
STATE: NOSTON
STATE: NOSTON
STATE: NOSTON
MEDIUM TYPE: Floppy disk
COMPUTER: TEM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PECENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA: 814
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.

TELECOMMATICATION INFORMATION:
NAME: (617) 248-7000
TELERCAN (617) 248-7000
TELERCAN (617) 248-7000
TELENGTH: 18 antino acide
STRANDENESS: single
TOPOLOGY: linear
MOLECULE TYPE: PEPTIGE
NAME/KEY: PEPTIGE
NAME/K
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07601
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                                                                                                                                                                                                                                                                               Sequence 8, Application US/08485948
Patent No. 5855882
CENERAL INFORMATION:
APPLICANT: YONG MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: ANTHONY CERAM:
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
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                                                           Length 18;
                                                         Query Match 93.0%; Score 66; DB 1; Length 18; Best Local Similarity 91.7%; Pred. No. 5.4e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHIR Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.0%; Score 66; DB 2; I 91.7%; Pred. No. 5.4e-05;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION WUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Hackensack
New Jersey
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OTHER INFORMATION: (20-37)"
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DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; FRAGMENT TYPE: internal US-08-485-948-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFOWDENIMRKVR 12
                                                                                                                                             1 CFOWQENMRKVR 12
                                                                                                                                                                                 1 CFOWORNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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US-08-204-487-3
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1 CFOWORNMRKVR 12

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HAPLOTYPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                      ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                     ALTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
RECISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMUNICATION INFORMATION:
TELEPHONE: 201 489-5800
TELEPHAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application US/07755161A Patent No. 5304633 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                        CLASSIFICATION:
PARIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWQENMRKVR 12
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U.S.A.
                                                                                           USA
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                                                                                                                                                                                                                                                          FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-07-755-161A-3
                                                                                           COUNTRY:
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Matches
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cyg regidue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys regidue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
SUFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY:
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FILING DATE:
PRILOND DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
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                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
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LOCATION: 2
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: Sir
TOPOLOGY: linear
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
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UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE TYPE:
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93.0%; Score 66; DB 1; Length 20;

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NAME/KEY: modified site
LOCATION: 19
LOCATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
PUBLICATION INFORMATION:
LOCATION: 2
IDENTIFICATION METHOD:
OTHER INPORMATION: //note= "thiol group of OTHER INFORMATION: //note= "thiol group of oTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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APPLICANT: YAMMOTO, NAOKI
APPLICANT: YAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANARA, SHIGEAKI
APPLICANT: TANARA, SHIGEAKI
APPLICANT: TAMASAKI, YOSHININ
APPLICANT: VAMASAKI, YOSHININ
TITLE OF INVENTION: UNIBLITORS
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATERT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: ATHERATIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 66, DB 1; Length 20;
Pred. No. 6e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REBERENCE DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08204487; Sequence 1, Application US/08204487; Patent No. 5565425; GENERAL INPORMATION: APPLICANT: NAKASHIMA, HIDEKI APPLICANT: MOSUCHI, WATARU APPLICANT: TANAKA, SHIGBAKI APPLICANT: KAWASAKI, YOSHIHIRO APPLICANT: UCHIDA, TOSHIAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              93.0%;
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Best Local Similarity 91.7
Matches 11; Conservative
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CLASSIFICATION:
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STREET: 53
CITY: BOST
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                                                                                                                                                                                                                                                                                                                               TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 7
US-08-204-487-1
                                                                                                                                                                                                                                                                                                           AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                        VOLUME:
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                                                                 Gaps
                                                                 ó
                                                                 1; Indels
                                                                                                                                                                                                                                          Sequence 3, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington
                                             91.7%; Pred. No. 6e-05;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warren M. Cheek Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMINICATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-371-8856
                                                                     11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN:
INDIVIDUAL ISOLATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POSITION IN GENOME:
CHROMOSOME/SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
                                                                                                            1 CFQWQENMRKVR 12
                                                                                                                                             2 CFQWQRNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: D.C. COUNTRY: U.S.A.
                                               Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAP POSITION
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                                                                                                                                                                                                                  RESULT 6
US-07-891-174-3
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93.0%; Score 66; DB 1; Length 20; 91.7%; Pred. No. 6e-05;
                                                                                   0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Wordberfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/;
FILING DATE: Ully 22, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
                                                                                                                       1 CFQWQENMRKVR 12
                                                                                                                                                        2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWQENMRKVR 12
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                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U.S.A.
                                                                                                                                                                                                                  RESULT 9
US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
       US-08-256-771-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
US-08-381-984-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24, Application US/08256771
Patent No. 5656591
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                            93.0%; Score 66; DB 1; Length 20; 91.7%; Pred. No. 6e-05;
                                                                                                                                                                                                                                                                                                                                 1; Indels
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                              ) LUCATION: 1..20

) OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE

) OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"

US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/256,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPRENCE/DOCKET UNBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/25
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24:
TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                               20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                 Matches 11; Conservative
                                                                                 TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                          NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                     1 CFOWQENMRKVR 12
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US-08-256-771-24
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                                                           LENGTH:
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Sequence 25, Application US/08256771
Patent No. 5655591
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
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US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
93.0%; Score 66; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IRM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                     COUNTY: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 STAY: Washington COUNTY: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/256,771
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TITLE OF INVENTION: amay production method of lactoferrin polypeptide from yeast and TITLE OF INVENTION: useful microorganism thereof TITLE OF INVENTION: useful microorganism thereof TITLE OF INVENTION: useful microorganism thereof CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: US/09/00373

PRIOR PELLING DATE: 1999-07-14

PRIOR PELLING DATE: 1998-07-14

PRIOR PELLING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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805 Fifteenth Street, N.W., #700
                                                                                                                               Diskette, 3.5 inch, 1.44 mb
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIPFICATION: 252
PRICR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-508-734-4; Application US/09508734; Patent No. 6423509
                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 amino acida
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: peptide
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                      Washington
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                                                             XY: U.S.A.
20005
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                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX:
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Best Local S
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OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 66; DB 1; Length 20; Pred. No. 6e-05;
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                                                                                                                                                                                                                                                                                 COMPUTER FRADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OFRATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
                         Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamorul TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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; Sequence 25, Application US/08381984
; Patent No. 5804555
; GENERAL INFORMATION:
    TITLE OF INVENTION: ANTIOXIDANT
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
      Sequence 24, Application US/08381984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CFÓWORNMRKVR 13
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                 STREET: 805 Fifte CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                 U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
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LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: (Anote= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4"
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OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
    FILING DATE:
ATTORNEY/AGENT INFORMATION:
ATMER WATTEN N. Cheek Jr.
REGISTRATION NUMBER: 33,367
                                                                                         REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: AMINO ACID STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified site LOCATION: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                      TELEPHONE: 202-371-885
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 4
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFOWDENMRKVR 12
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                                                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11.
MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-07-755-161A-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN:
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APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR APPLICATION NUMBER: KR1998-29351
NUMBER OF SEQ ID NOS: 12
SOFTWARE: KopatentIn 1.71
SEQ ID NO 6
LENGTH: 24
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93.0%; Score 66; DB 4; Length 24;
Best Local Similarity 91.7%; Pred. No. 7.2e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                             Query Match

93.0%; Score 66; DB 4; Length 22;
Best Local Similarity 91.7%; Pred. No. 6.6e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
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Sequence 10, Application US/07755161A
Sequence 10, Application US/07755161A
Sexuent No. 5304633
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Disnlarvari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Wenderoth, Lind & Ponack
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                    Sequence 6, Application US/09508734 Patent No. 6423509
LENGTH: 22
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT; CAGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Wenderc
STREET: 805 Fiftee
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                  1 CFOWDENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CFOWQENMRKVR 12
                                                                                                                                                                                                                                           2 CFOWORNWRKVR 13
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                                                                    US-09-508-734-4
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FEATURE:
NAME/KEY: modified site
LOCATION: 4
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                        GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 09-DATA:
APPLICATION NUMBER: US/07/55,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WARTEN M. Cheek JT.
REGISTRATION NUMBER: 33,367
US-07-891-174-10
; Sequence 10, Application US/07891174
; Patent No. 5317084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRATURE:
NAME/KEY: modified site
LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                             STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
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MOLECULE TYPE:
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DEBUTIFICATION METHOD:

COTHER INFORMATION: Chote= "thiol group of connected by disulfide bond with cother information: Cys residue at location 4"

PUBLICATION INFORMATION:

AUTHORS:

TITLE:

JOUGHES:

JOCHER INFORMATION:

AUTHORS:

TITLE:

JOCHER INFORMATION:

AUTHORS:

TITLE:

JOCHER INFORMATION:

PUBLICATION INFORMATION:

PAGES:

DATE:

JOCHER INFORMATION:

MATCHES:

JOCHER INFORMATION:

MATCHES:

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AUTHORS:

MATCHES:

JOCHER INFORMATION:

MISMATCHES:

MATCHES:

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DATE:

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MATCHES:

DD 4 GFOWQRNWRKVR 12

JOCHER MATCHES:

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February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec
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1: \cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*

2: \cgn2_6/fycodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: \cgn2_6/fycodata/2/pubpaa/USO6_NEW_PUB.pep:*

4: \cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

5: \cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*

6: \cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*

7: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

7: \cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

8: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

9: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

10: \cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep:*

11: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

11: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

13: \cgn2_6/ptodata/2/pubpaa/USO9_PUBCOMB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*

14: \cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 156504 seqs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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71
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 2, Appli Sequence 20, Appli Sequence 3, Appli Sequence 3, Appli Sequence 23, Appli Sequence 24, Appli Sequence 26, Appli Sequence 27, Appli Sequence 28, Appli Sequence 30, Appli Sequence 30, Appli Sequence 58, Appli Sequence 28, Appli
SUMMARIES	US-09-798-869-2 US-00-798-869-20 US-00-798-869-20 US-09-798-869-3 US-09-798-869-3 US-09-798-869-7 US-09-798-869-7 US-09-798-869-7 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-09-798-869-8 US-10-066-273-58 US-10-066-273-58 US-10-066-273-58 US-10-066-273-58 US-09-976-165-28
DB	; ; о о о о о о о о о о о о о о о о о о
% Query Match Length	0.09 0.09 0.09 0.09 0.09 0.09 0.09 0.09
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Sequence 12, Appl Sequence 10, Appl Sequence 40025, A	Sequence 5, Appli Sequence 244, App		121	130	Sequence 43, Appl	'n	Sequence 5, Appli	Ò	9	Ñ	Sequence 25, Appl	Sequence 1, Appli	H	Sequence 28, Appl	Sequence 24, Appl	Sequence 21, Appl	Sequence 4, Appli	• •		Sequence 46393, A
US-09-995-542-12 US-09-995-542-10 US-09-864-761-40025	9-7	US-09-945-301-11 US-09-879-957-194	- 60	US-09-815-242-13026	US-09-771-730-43	-738-626-	US-10-135-322-5	US-10-135-322-24	US-09-918-508-6	US-09-798-869-26	US-09-798-869-25	US-09-798-869-1	US-09-798-869-10	US-09-798-869-28	US-09-798-869-24	US-09-798-869-21	US-09-909-652-4	US-09-030-619-205	US-09-917-340-16	US-09-864-761-46393
100	9	10	10	10	10	σ	σ	σ	σ	σ	σ	σ	0	0	6	σ	10	10	10	10
2273 2310 33	119	302 509	70	62	321	943	1057	1057	1057	13	14	15	15	15	18	25	25	25	25	40
52.1 52.1 50.7	49.3	49.3	48.6	47.9	47.9	47.9	47.9	47.9	47.9	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5	46.5
37 37 36	35	3 3 5	34.5	3.4	34	34	34	34	34	33	33	33	33	33	33	33	33	33	33	33
20 21 22	23	25 26	27	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Gaps
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                                                                                                                       APPLICANT: BALDUR SYRINBJ (RNSSON APPLICANT: LARS VORLAND TITLE OF INVENTION: BIOACTIVE PEPTIDES FILE REFERENCE: A34049-PCT-USA-A CURRENT FILING DATE: 2001-02-27 PRIOR APPLICATION NUMBER: US/09/798,869 PRIOR FILING DATE: 1999-08-31 PRIOR FILING DATE: 1999-08-31 PRIOR PLING DATE: 1998-08-28
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 30 SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
               Sequence 2, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ(RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11; Conservative
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US-09-798-869-2
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Best Local Similarity
Matches 11; Conserv
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US-09-798-869-20
US-09-798-869-2
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LENGTH: 15
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93.0%;
91.7%;
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Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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                                                                               1 CFOWDENMRKVR 12
                                                                                                                   22 CFOWORNMRKVR 33
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US-09-798-869-3
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LENGTH: 15
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Patent No. US20020160941A1
CENERAL INFORMATION:
APPLICANT: Kurecki, Tomasz
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                          93.0%; Score 66; DB 9; Length 25; 91.7%; Pred. No. 0.00011; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W. CITY: Washington D.C. COUNTRY: U.S.A.
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34040-PCT-UGS-A
FILE REFERENCE: A34040-PCT-UGS-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOTTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-WAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REPERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 393-5350 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFOWDENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 CFOWORNWRKVR 14
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OPERATING SYSTEM:
SOFTWARE: PatentI
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US-10-023-096-2
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Description of the conservative of the conserv
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63.4%; Score 45; DB 9; Length 15; 63.6%; Pred. No. 0.17; 1ive 1; Mismatches 3; Indels
                                                                                                                                                                                                         APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: HALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFRENCES: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1099-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
RIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRABLSEQ FOR WINDOWS VETSION 4.0
                                                                                                                                             Sequence 4, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
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Best Local Similarity 63.63
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 63.4
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWDENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 CLRWQNEMRKV 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 CLRWONEMRKV 13
1 CFOWDENMRKV 11
                       3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: MURINE
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.0%; Score 49; DB 9; Length 25; 63.6%; Pred. No. 0.062; 2; Indels tive 2; Mismatches 2; Indels
2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09798869;
Publication No. US2030022821A1;
GRERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT PILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-3
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASELED OF WINGOWS VERSION 4.0
                                                                                                                                                             WESULY 6

US-09-798-869-23

Sequence 23, Application US/0979869

Publication No. US20030022821A1

GENERAL INFORMATION:

APPLICANT: (YSTEIN REKDAL

APPLICANT: LAKS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 1999-08-31

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 25
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 63.6
Matches 7; Conservative
7; Conservative
                                         1 CFOWQENMRKV 11
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                                                                                   3 CYÓWORRMRKL 13
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; ORGANISM: CAPRINE
US-09-798-869-23
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Matches
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63.6%; Pred. No. 0.27;
iive 1; Mismatches
US-09-798-869-22
Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: (YSTEIN REKDAL
APPLICANT: HYSTEIN REKDAL
APPLICANT: HYSTEIN REKDAL
APPLICANT: HYSTEIN REKDAL
APPLICANT: HYSTEIN SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALOUR SVEINBJ (RNSSON
APPLICANTION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-0C-27
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASESEQ for Windowe Version 4.0
SEQ ID NO 22
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APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
TYPING OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798, 669
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
Sequence 30, Application US/09798869 Publication No. US20030022821A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQENMRKV 11
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Matches 6; Conserv
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US-09-798-869-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.2%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.51; tive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 42; DB 9; Length 15;
Pred. No. 0.51;
1; Mismatches 3; Indels
                                     JOS-09-798-89-89

JOS-09-798-89-89

Publication No US20030022821A1

GENERAL INFORMATION:

APPLICANT: GOIN SIGHED SYENDEN

APPLICANT: HARS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT APPLICATION NUMBER: CTG/0899/02851

PRIOR PILING DATE: 1999-08-31

PRIOR FILING DATE: 1998-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 8

LENGTH: 15

CORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOS-09-798-889-29

JOS-09-798-889-29

Publication No. US20030022821A1

GENERAL INFORMATION:

APPLICANT: JOHN SIGHED SVENDEN

APPLICANT: (YSTEIN REKDAL

APPLICANT: BALDUR SVEINBU (RNSON

APPLICANT: LARS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

FILE REFERENCE: A34049-PCT-USA-A

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: PCT/GB99/02851

PRIOR APPLICATION NUMBER: GB9918938.4

PRIOR APPLICATION NUMBER: GB918938.4

PRIOR FILING DATE: 1999-08-28

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 29

LENGTH: 15
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Best Local Similarity 54.5%,
E.a. 6; Conservative
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Best Local Similarity 63.6'
Matches 7; Conservative
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US-09-798-869-29
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GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Sharron G.
APPLICANT: Penn, Wensheng
TITLE De INVENTION INFORMATION:
TITLE OF INVENTION INVERS: US 60/180,312
PRIOR APPLICATION WINDER: US 60/180,312
PRIOR APPLICATION WINDER: US 60/200,466
PRIOR APPLICATION WINDER: US 60/200,466
PRIOR APPLICATION WINDER: US 60/200,466
PRIOR PILING DATE: 2000-00-20
PRIOR PILING DATE: 2000-00-20
PRIOR PILING DATE: 2000-00-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE:
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59.2%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.51; 2; Indels tive 3; Mismatches 2; Indels
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; Patent No. US20020048763A1
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RESULT 12 US-09-798-869-30

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.9

OTHER INFORMATION: EXPRESSED IN HERAT, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN PLACENIA, SIGNAL = 0.81

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN BOLT LIVER, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN BOLT LIVER, SIGNAL = 0.75

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 0.76

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 0.84

OTHER INFORMATION: EXPRESSED IN HELLOO, SIGNAL = 0.84

OTHER INFORMATION: SYMESSED IN HELLOO, SIGNAL = 0.84

OTHER INFORMATION: SYMESSED IN HELLOO, SIGNAL = 0.84

OTHER INFORMATION: SWISSPROT HIT: P1678113.1, EVALUE 1.00e-100

US-09-864-761-37353
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PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR FILING DATE: 2001-01-30
PRIOR PELICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR PILING DATE: 2001-01-29
PRIOR PILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO 37353
LENGTH: 239
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APPLICANT: Avin P. Baker APPLICANT: Kevin P. Baker APPLICANT: David A. Botstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nicholas F. Paoni
Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Paul J. Godowski
Austin L. Gurney
Ivar J. Kljavin
Jennie P. Mather
Mary A. Napier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colin K. Watanabe
P.Mickey Williams
William I. Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Luc Desnoyers
Dan L. Eaton
Napoleone Ferrara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mary E. Gerritsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sherman Fong
Wei-Qiang Gao
Hanspeter Gerber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Goddard
                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       James Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQENMRKV 11
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APPLICANT:
APPLICANT:
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APPLICANT:
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PRIOR FILING DATE: 1997-10-29
PRIOR FILING DATE: 1997-10-29
PRIOR PAPPLICATION NUMBER: 09/136801
PRIOR PLING DATE: 1998-08-19
PRIOR PAPPLICATION NUMBER: 09/136801
PRIOR PAPPLICATION NUMBER: 09/136804
PRIOR PLING DATE: 1998-08-19
PRIOR PLING DATE: 1998-09-19
PRIOR PLING DATE: 1998-09-19
PRIOR PLING DATE: 1998-09-19
PRIOR PLING DATE: 1998-09-19
PRIOR PLING DATE: 1998-09-10
PRIOR PAPLICATION NUMBER: 09/18097
PRIOR PLING DATE: 1999-09-10
PRIOR PAPLICATION NUMBER: 09/24460
PRIOR PLING DATE: 1999-03-09
PRIOR PLING DATE: 1999-04-15
PRIOR PLING DATE: 1999-06-14
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Best Local Similarity 45.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 3; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR APPLICATION NUMBER: PCT/US98/25109
PRIOR PLILING DATE: 1998-11-20
PRIOR PLILING DATE: 1998-11-20
PRIOR PLILING DATE: 1998-11-25
PRIOR PLILING DATE: 1999-10-01
PRIOR PLILING DATE: 1999-0-10
PRIOR PLILING DATE: 1999-0-0-0
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PRIOR APPLICATION NUMBER: PCT/US99/2051
PRIOR PLILING DATE: 1999-0-0-0
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR APPLICATION NUMBER: PCT/US99/21547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/056974
PRIOR FILING DATE: 1997-08-26
PRIOR APPLICATION NUMBER: 60/059115
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Margaret Ann Roy
Timothy A. Stewart
Daniel Tumas
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Dan L. Baton
Napoleone Ferrara
Sherman Fong
Wei-Qiang Gao
Hanspeter Gerber
Mary E. Gerritsen
Audrey Goddard
Paul J. Godowski
Austin L. Gurney
Jean F. Kljavin
Jennie P. Mather
Mary A. Napier
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Avi J. Ashkenazi
APPLICANT: Kevin P. Baker
APPLICANT: David A. Botstein
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PRIOR FILING DATE: 1997-09-17
PRIOR PELICATION NUMBER: 60/06285
PRIOR APPLICATION NUMBER: 60/06285
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PRIOR FILING DATE: 1997-10-24
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PRIOR FILING DATE: 1997-10-24
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PRIOR APPLICATION NUMBER: 60/06343
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PRIOR APPLICATION NUMBER: 60/06964
PRIOR PILING DATE: 1997-11-26
PRIOR PLING DATE: 1997-11-26
PRIOR APPLICATION NUMBER: 60/069694
PRIOR PILING DATE: 1998-02-09
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PRIOR PLING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-09
PRIOR PLING DATE: 1998-03-09
PRIOR PLING DATE: 1998-04-08
PRIOR PLING DATE: 1998-08-18
                                      APPLICATION NUMBER: 60/059588
FILING DATE: 1997-09-17
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APPLICATION NUMBER: 60/100858
FILING DATE: 1998-09-17
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FILING DATE: 1999-03-23
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APPLICATION NUMBER: 60/145070
FILING DATE: 1999-07-20
APPLICATION NUMBER: 60/145698
FILING DATE: 1999-07-26
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APPLICATION NUMBER: 60/099811
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FILING DATE: 1998-09-24
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FILING DATE: 1998-10-28
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FILING DATE: 1999-06-15
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FILING DATE: 1999-12-07
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FILING DATE: 1997-08-26
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APPLICATION NUMBER: 09/136801
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FILING DATE: 1998-08-19
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FILING DATE: 1997-09-18
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PRIOR PLICATION NUMBER: 09/180397
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PRIOR PLING DATE: 1998-09-01
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PRIOR PLING DATE: 2001-0-18
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PRIOR PRILCATION NUMBER: PCT/US98/19330
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Search completed: February 21, 2003, 08:08:09 Job time: 11.55 secs

1 CFQWQENMRKV 11 | :|| | |: 311 CVRWQINSRRI 321

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55 ; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-85 71 1 CFQWQENMRKVR 12 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pir1:*
2: pir2:*
3: pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

translation elonga	translation elonga	translation elonga	DNA excision-repai	hypothetical prote		hypothetical prote	hypothetical prote	hypothetical prote	. lipoprotein [impor	hypothetical prote	Mtr/TnaB/Tyro perm	hypothetical prote	hypothetical prote	hypothetical prote	
EFHU2	EFRT2	A25440	A56213	D64388	D64935	B85785	F90936	T27145	A99515	AD2346	C81729	T45825	T45824	T46261	D84588
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53.5	53.5	53.5	53.5	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1	52.1
38	38	38	38	37	37	37	37	37	37	37	37	37	37	37	37
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

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A; Molecule type: mRNA
A; Residues: 1-711 < CHO
A; Rosidues: 1-711 < CHO
A; Residues: 1-711 < CHO
A; Cross-references EMBL: U07643; NID:9467236; PIDN:AAB60324.1; PID:9467237
A; Residues: 1-711 < CHO
A; Rikey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A; Rike complete nuclectide sequence of human mammary gland lactoferrin.
A; Reference number: S11228; MUID:90384839; PMID:2402455
A; Reference number: S11228; MUID:90384839; PMID:2402455
A; Reference number: BRNA
A; Residues: 1-148, T',150-422, C', 424-711 < REY>
A; Residues: 1-148, T',150-422, C', 424-711 < REY>
A; Residues: EMBL:X53861; NID:934415; PIDN:CAA37914.1; PID:934416
B; Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocratinol. 6, 1969-1981, 1992
A; Reference number: A45401; MUID:93125571; PMID:1480183
                                                  N,Alternate names: lactoferrin
C,Species: Homo sapiens (man)
C,Datecies: Homo sapiens (man)
C,Datecies: J-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C,Accession: G01394; S11228; Ā45401; S10324; S15853; S20841; S07160; A61169; A31000; S74
                                                                                                                                                                                                                              R,Cho, Y.

Submitted to the EMBL Data Library, March 1994
A,Reference number: G06820
A,Accession: G01394
A,Status: preliminary; translated from GB/EMBL/DDBU
lactotransferrin precursor [validated] - human
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A; Accession: A45401

A; Molecule type: DNA
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A; Residues: 1-15 <TEN>
A; Residues: 1-15 <TEN>
A; Crosq.-references: GB: S52659; NID: g263311; PIDN: AAB24877.1; PID: g263312
A; Experimental source: placenta
A; Note: sequence extracted from NCBI backbone (NCBIP: 122202)
A; Note: sequence extracted from NCBI backbone (NCBIP: 122202)
A; Note A; Note A; Ogden, U.B.
A; Title: Nucleotide sequence of human lactoferrin cDNA.
A; Reference number: S10324; MUID: 90326549; PMID: 2374734

A; Molecule type: mRNA A; Residues: 3-711 < POW> A; Accession: S10324

A;Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem J. 276, 349-3155, 191
A;Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066

A; Accession: S15853

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 20-31 <ST1>

A; Accession: S20841

A;Molecule type: protein A;Residues: 20-28,'X',30-31 <ST2>

Length 33;

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DB 2;
   Score 50;
Pred. No. (
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   70.48;
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A;Residues: 3-707 <PEN>
A;Cross-references: EMBL:J03298
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Best Local Similarity 63.5-
Fering 7; Conservative
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Matches 7; Conservative
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A; Residues: 1-15 <LIU>
A; Cross-references: GB:M74778
                                                                       7; Conservative
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Query Match
Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-708 <LEP>
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                                                                   Matches
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                                                                                                                                                                A,Molecule type: mRNA
A,Residues: 436-487, 'A',489-711 <RAD>
A,Residues: 436-487, 'A',489-711 <RAD>
A,Residues: 436-487, 'A',489-711 <RAD>
A,Cross-references: EMBL:M18642; NID:G186815; PIDN:AA86665.1; PID:G386855
R,Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A,Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A,Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: not compared with conceptual translation
A;Ratus: not compared with conceptual translation
A;Residues: 3-701,'SWKPVN' <PAN>
A;Residues: 3-701,'SWKPVN' <PAN>
A;Experimental source: normal breast tissue
B;Metz-Boutigue, M.H.; Joiles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Bur. J. Biochem. 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth A;Reference number: A31000; MUID:85076667; PMID:6510420
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 899-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR
A;Reference number: S07160; MUID:88001031; PMID:3477300
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7-1-19/Domain: signal sequence #status predicted <SIG>
7-1-19/Domain: signal sequence #status predicted <SIG>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;39-65,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157,498/Rhinding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
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A; Molecule type: protein
A; Mesidues: 20-140,142-1169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-A; Mesidues: 20-140,142-1169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-R; Molec: this is the final paper in a series
R; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
B; Hoegdall, E.V.; Barkholt, V.; Norskov, L.
A; Hoegdall, E.V.; Barkholt, V.; Molecon, Sandall, Br. Grant and purification by aminohexyl affile is actoferrin: similarity to diamine oxidase and purification by aminohexyl affile A; Reference number: S74119; MUID:97054624; PMID:8899821
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R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Bjochim, Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: S52107; MJID:95127729; PMID:7827104
A;Accession: S52107
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C,Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C,Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
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Pred. No. 0.0016;
0; Mismatches 1; Indels
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C;Superfamily: transferrin; transferrin repeat homology
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
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A;Cross-references: GDB:119368; OMIM:150210
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Best Local Similarity 91.7%;
Matches 11; Conservative
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lactoferrin precursor - mouse
NiAlternate names: lactotransferrin
C;Spales Mus musculus (house mouse)
C;Spales: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A28438; A41205
C;Accession: A28438; A41205
J; Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secritise incompler: A92596; MUID:87280033; PMID:3611056
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C;Reywords: duplication; glycoprotein
F;355-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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J. Biol. Cham. 266, 21880-21885, 1991
Afritle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                         CiSpecies: Capra aegagrus hircus (domestic goat)
CiDate: 20-Peb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
CiAccession: JC2323
Rice Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biochem. Baschem. 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the reA;Ference number: JC2323; MUID:94380047; PMID:8093048
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F;20-707/Product: lactotransferrin #status predicted <MAT>
F:388-695/Domain: transferrin repeat homology <FRH2>
F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 1.4;
2; Mismatches 2; Indel's
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1; Indels
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3; Mismatches
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RESULT 5

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hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Ty C; Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Pate: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
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R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serova; Reference number: AB0502; PMID:11677608
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C;Genetics:
A;Gene: STY3070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: Z81089; PIDN: CAB03137.1; GSPDB: GN00028; CESP: F53H4.4
hypothetical protein F53H4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
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A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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                                                                                                                                                                                                                                                            A,Reference number: 219587
A,Accession: T22597
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                     R,Dobson, R. submitted to the EMBL Data Library, October 1996
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Best Local Similarity 63.6-
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262 FQWKISMRKTR 272
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A;Molecule type: DNA
A;Residues: 1-511 <PAR>
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Matches 7; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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A;Residues: 1-275 <W
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                                                                                                                                                                                                                            C.Accession: T08030
R.Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: Z16302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A.Map position: IX
A.Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3
3334/3; 3686/3; 3882/3; 4240/3
C; Superfamily: dynein heavy chain, ciliary
C; Reywords: nucleotide binding; P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
F;25202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C'Accession: G86403
R'Theologis, A.; Ecker, U.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huzar, L.
Abature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Reference number: A86141; WUID:21016719; PMID:11130712
A; Scatture preliminary
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A;Residues: 1-289 <STO>
A;Cross-references: GB:AE005172; NID:g10998925; PIDN:AAG26065.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                     dynein beta heavy chain - Chlamydomonas reinhardtii
C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Accession: T08030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-4568 <MIT>
A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
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63.4%; Score 45; DB 2; Length 4568; 50.0%; Pred. No. 48; 3; Indels tive

Conservative

9

Matches

ò

Query Match Best Local Similarity

A; Experimental source: strain 21gr

A;Gene: ODA4

33.3K hypothetical protein F28L5.13 - Arabidopsis thaliana

59.2%; Score 42; DB 2; Length 289; 58.3%; Pred. No. 9.2; ive 1; Mismatches 4; Indels

ilarity 58.3%; Conservative

Local Similarity Les 7; Conserv

Best Loca Matches

Query Match

1 CFQWQENMRKVR 12 CFTWEEYARHVR 19

RESULT 7

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Query Match 54.9%;
Best Local Similarity 58.3%;
Matches 7; Conservative
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A;Map position: linear chromosome
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A;Gene: Atu4566
A;Map position: linear chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 8/...
7; Conservative
                                                                                                                                                                                                                                                                                                                                         158 CFGKKENMROMR 169
                                                                                                                                                                                                                                                                                       1 CFQWQENMRKVR 12
        A;Residues: 1-267 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 WQENWRYV 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 WQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                   A; Genetic code: SGC3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: E98169
                                                                                                        Genetics:
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AB3118
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A,Cross-references: EMBL:Z74053; NID:g1430962; PIDN:CAA98561.1; PID:e252970; PID:g143096
A,Experimental source: strain S288C
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C;Date: 09-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-Dec-1999
C;Date: 09-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-Dec-1999
C;Date: 09-Oct-1997 #sequence_revision 31-Oct-1997 #text_change 07-Dec-1999
R;Bork, Ouzounis, C; Casari, G; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.;
Mol. Microbiol. 16, 955-967, 1995
A;Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiold
A;Reference number: S77739; MUID:96059641; PMID:7476192
                     A;Cross-references: GB:AE001354; GB:AE001273; NID:g3329280; PIDN:AAC68414.1; PID:g332928
A;Experimental source: serotype D, strain UW-3/Cx
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A; Readules: 1-431 < must
A; Readules: 1-431 < must
A; Cross-references: EMEL: Z48008; NID: g642799; PIDN: CAA88056.1; PID: g642801
B; Andre, B.; Vissers, S.; Urrestarazu, L.
Submitted to the EMBL Data Library, February 1995
A; Description: The sequence of a 42 kb segment located on the left arm of chromosome A; Reference number: S52492
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S50977
hypothetical protein YDL005c - yeast (Saccharomyces cerevisiae)
N.Alternate names: hypothetical protein D2930; hypothetical protein YD8119,02c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Saccharomyces cerevisiae
C;Date: 11-Feb-1995 #sequence revision 12-May-1995 #text_change 19-Apr-2002
C;Accession: S50977; S52514; S67537
R;Murphy, L.; Richards, C.; Gentles, S.; Harris, D.
A;Reference number: S50976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,Cross-references: EMBL:Z48432; NID:g683669; PIDN:CAA88354.1; PID:g683692 R;Urrestarazu, L.A.; Andre, B.; Vissers, S. submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                   Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.3%; Score 40; DB 2; Length 431; 100.0%; Pred. No. 31; cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                    3; Indels
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hypothetical protein MC003 - Mycoplasma capricolum (fragment)
                                                                                                                                                                              Score 40; DB 2;
Pred. No. 30;
                                                                                                A,Gene: tyrP_1 C,Superfamily: tyrosine-specific transport protein
                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                           h 56.3%;
Similarity 70.0%;
7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Gene: SGD:MED2
A,Cross-references: SGD:S0002163
A,Map position: 4L
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                                                                                                                                                                                                                                                                                                                                 317 FOWDEKKRKV 326
                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                 2 FOWQENMRKV 11
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A; Residues: 1-431 <AND>
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Best Local Similarity
Matches 8, Conserv
A;Residues: 1-415 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 QENMRKVR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
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                                                                           C;Genetics:
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C; Accession: E98169
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman
A; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 201
A; Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A; Reference number: A97359; PMID:11743194
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C;Species: L1-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
C;Accession: AB3118
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, Errage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel science 294, 2317-2323, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A, Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       serine proteinase Atu4566 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            serine proteinase XF0267 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002
A;Cross-references: EMBL:Z33006
A;Experimental source: ATCC 27343
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ster, E.W.

Yittle: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; PMID:11743193

A;Accession: AB3118
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A,Molecule type: DNA
A,Residues: 1-660 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK88879.1; PID:g15158646; GSPDB:GN00170
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Residues: 1-60 «KOR»
A,Cross-references: GB:AE008689; PIDN:AAL45360.1; PID:g17743054; GSPDB:GN00187
A,Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                           Score 39; DB 2; Length 267; Pred. No. 28; 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Length 660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   54.9%; Score 39; DB 87.5%; Pred. No. 72;
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4 WQENMRKV 11

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A;Geme: CBSP:C24H11.8
A;Map position: 3
A;Introns: 18/3; 65/3; 108/1; 138/1; 177/3; 256/2; 303/2; 343/1; 409/3; 484/3; 532/2; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA la protein - broad bean mottle virus (strain Bawden)

N;Contains: ATP-dependent helicase (EC 3.6.1.-); mRNA (guanine-N7-)-methyltransferase (EC;Species: broad bean mottle virus

C;Species: broad bean mottle virus

C;Species: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 19-Jan-2001

C;Accession: A41699

R;Drianott, A.M.; Bujarski, J.J.

N;Cology 185, 553-562, 1991

A;Title: The nucleotide sequence and genome organization of the RNA-1 segment in two broad A;Reference number: A41699; MUID:92074218; PMID:1962437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Accession, maion RNA
A;Residues; 1-966 <DZI>
A;Residues; 1-966 <DZI>
A;Residues; 1-966 <DZI>
A;Cross-references: GB:M65138; NID:g210662; PIDN:AAA42740.1; PID:g210663
A;Cross-references: GB:M65138; NID:g210662; PIDN:AAA42740.1; PID:g210663
C;Superfamily: cucumber mosaic virus RNA 1 protein
C;Keywords: hydrolase; methyltransferase; mRNA capping; nucleotide binding; P-loop; S-ad
F;80-168/Domain: methyltransferase #status predicted <MTF>
F;680-697/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                    A;Reference number: Z19123
A;Accession: T19429
A;Scaliniary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-681 «WIL»
A;Cross-references: EMBL:Z81475; PIDN:CAB03914.1; GSPDB:GN00021; CESP:C24H11.8
A;Experimental source: clone C24H11
                                                                                                                                                               hypothetical protein C24H11.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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R,Lloyd, C.
submitted to the BMBL Data Library, November 1996
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Best Local Similarity 60.0
Matches 6; Conservative
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          126 WOENMRYV 133
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Gaps

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:25:55; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec

US-09-743-107B-85 71 1 CFQWQENMRKVR 12 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0
Maximum DB seg length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt 40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Rest

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ALIGNMENTS

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1LCT; 31-OCT-93.
1LFG; 31-JUL-94.
1LFH; 31-OCT-93.
1LFI; 31-OCT-93.
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12-MAR-97.
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 McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D., Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K., Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D., Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M., Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U., Diaz-Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D., Sagripanti J.L.;
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"Mol. Biol. 209:711-734 (1989).
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                                                                                                                                                                                                                                                     alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains. ";
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Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
                                                                                                                                                                                                                                                                                                                                 Metz-Boutigue M.-H., Jolles J., Mazurier J., Spik G., Montreuil J.,
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Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Rado T.A., Wei X., Benz E.J. Jr., "Isolation of lactoferrin cDNA from a human myeloid library an expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                  SEQUENCE OF 20-711.

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"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
                                                                                                                                                                                       PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS), AND REVISIONS.
                                                                                                                                                                                                                                                                                                                                           Jolles P.;
"An 88 amino acid long C-terminal sequence of human
                                   Powell M.J., Ogden J.E.; "Nucleotide sequence of human lactoferrin cDNA.";
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MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
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          TIŠSUB=Mammary gland;
MEDLINE=90326549; PubMed=2374734;
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 436-711 FROM N.A.
MEDLINE-88001031; PubMed=3477300;
                                                                                                                                                                                                                                                                                                                  MEDLINE=82262043; PubMed=7049727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253-->methionine mutant.";
Biochemistry 36:341-346(1997).
                                                                                                                                                                                                                                                                                                                                                                               FEBS Lett. 142:107-110(1982).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 237-711 FROM N.A.
3-711 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOFERROXIN A SHOWS PREFERRNCE FOR MU-RECEPPORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE FOR KAPPA-RECEPPORS THAN FOR MU-RECEPPORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H., Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=9873069;
Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,
Quasiyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y.,
Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,
Bl Matri L., Iwata F., Kaiser-Kupfer M., Nagata M., Nakayasu K.,
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corneal dystrophy): exclusion of linkage to lactoferrin gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                 Acta Crystallogr. D 54:1319-1335(1998).
                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Agric. Biol. Chem. 54:1803-1810(1990).
                                                                                                           Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                           CHARACTERIZATION OF LACTOFERROXINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF332168; AAG48753.1; -. EMBL; BC015822; AAH15822.1; -. EMBL; BC015823; AAH15823.1; -.
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EMBL; M93150; AAA36159.1; --
EMBL; M83202; AAA59511.1; --
EMBL; M3205; AAA58656.1; --
EMBL; M18642; AAA8665.1; --
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X52941, CAA37116.1; -.
U95626, AAB57795.1; -.
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                                                                                                                                                                                                                                                        Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!-FUNCTION: TRANSFERRING ARE IRON BINDING TRANSFORT PROTEINS WHICH
CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!-SUBBLIT: MONOMER (BY SIMILARITY).
-!-SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!-SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Camelus dromedarius (Dromedary) (Arabian camel).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486 (1999).
                       .;
0
    Query Match 93.0%; Score 66; DB 1; Length 711; Best Local Similarity 91.7%; Pred. No. 0.00037; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                         BY SIMILARITY.
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MEDLINE=94380047; PubMed=8093048;
MEDLINE=94380047; PubMed=8093048;
MEDLINE=94380047; PubMed=8093048;

"Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine U12 synteny group.";

Biochem Biophys. Res. Commun. 203:1334-1332 [1994).

-I- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUBALLY BICARBONATE.
-I- SUBUNIT: MONOWER (BY SIMILARITY).
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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124 Q -> K (IN REF. 2).
154 F -> P (IN REF. 2).
304 S -> P (IN REF. 2).
414 D -> G (IN REF. 2).
414 D -> G (IN REF. 2).
417358 MW; F2EDBA3C83539960D CRC64;
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N-LINKED (GLONAC. . . )
-!- DOMAIN; COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN,
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Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANGFERRIN.
SMART; SM00094; TR PER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
                                                                                                                                              EMBL; U53857; AAA97958.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDULAR-SECTION OF SETTOGEN-RESPONSIVE MOUSE LACTOFERIN DIOMOCER.";
Liu Y., TEARACTERION OF SETTOGEN-RESPONSIVE MOUSE LACTOFERIN DIOMOCER.";
J. Biol. Chem. 266:21880-21885(1991).
-I. FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pentecost B.T., Teng C.T.;
"Lactotransferrin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases
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-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
TRFL MOUSE STANDARD; PRT; 707 AA. P08071; P70690; Q61799; Q922P2; P1-806-1988 (Rel. 08, Created) P1-507W-2002 (Rel. 41, Last sequence update) P15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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LACTOTRANSFERRIN.
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J. Biol. Chem. 262:10134-10139(1987).
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EMBL; D88510; BAA133.1; --
EMBL; BC006904; AAH06904.1; --
EMBL; MA4778; AAA39427.1; --
PIR; A28438; A28438
HSSP; P02788; LE6.
MGD; MGT:96837; Ltf.
InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
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SUBCELLULAR LOCATION: Secreted
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MEDLINE=87280033; PubMed=3611056;
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MEDLINE=92042099; PubMed=1939212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. MOI. BIOL. 289:303-317 (1999).
-1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS. OF PERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
-1- SUBUNIT: MONOMER.
-1- SUBCELLULAR LOCATION: Secreted.
-1- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-1- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eŭkaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Perissodactyla, Equidae, Equus.
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MICROTUBULE-BINDING (POTENTIAL).
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InterPro; IPRO04273; Dynein heavy.
Pfam; PF03028; Dynein heavy.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
Coiled coil.

277 293 COILED COIL (POTENTIAL)
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Pred. No. 15;
3; Mismatches 3; Indels
-1- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Isst annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
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ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GLCNAC. . .) (POTENTIAL). (GLCNAC. . .) (POTENTIAL).
                                                                                                             InterPro; IPR001156; Transferrin.
Pfan; PF00405; transferrin; 2.
PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR_FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 41; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07BB84D50E1B165D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                        IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                     LACTOTRANSFERRIN.
1.
2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           267 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED
N-LINKED
N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Y125 MYCCA STANDARD; ID VI25 MYCCA STANDARD; ID VI25 MYCCA STANDARD; ID VI-00T-1996 (Rel. 34, Created)
                                                                          EMBL, AJ010930; CAA09407.1; -. PDB; 1B1X; 02-DEC-98. PDB; 1B7U; 02-FEB-99. PDB; 1B7Z; 02-FEB-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57.7%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 58.3.,
7, Conservative
                                                                                                                                                                                   Signal; 3D-structure.
NON TER 1
SIGNAL <1
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| CAKFQRNMKKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         695 AA;
                                                                                                                                                                                                                                                                                          23337
3357
44811
44811
44831
648
631
668
631
4401
4401
433
                                                                                                                                                                                                                                                                                                                                                               DISULFID
DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              SINDING
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METAL
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METAL
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                                                                                                                                                                                                                                                                                                                                                its physiology.";
Mol. Microbiol. 16:955-967(1995).
-!- SIMILARITY: BELONGS TO THE COF/YBHA/YIDA/YICL (E.COLI) / YCSE/YXEH
(B.SUBTILIS) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dzianott A.M., Bujarski J.J., "The nucleotide sequence and genome organization of the RNA-1 segment in two bromoviruses: broad bean mottle virus and cowpea chlorotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THE
                                                                                                                                                                                                                                                                                                                              Exploring the Mycoplasma capricolum genome: a minimal cell reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in two bromoviruses: broad bean mottle virus and confidence.";
mottle virus.";
Virology 185:553-562(1991).
-!- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CONTAINS AN HELICASE DOMAIN AND A METHYLTRANSFERASE DOMAIN.
METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.9%; Score 39; DB 1; Length 267; 58.3%; Pred. No. 8.4; 2; Indels iive 3; Mismatches 2; Indels
                                                                                                                                                                                                                        STRAIN=ATCC 27343 / KID;
MEDDINES96059641; PubMeda-7476192;
BOTK P., Ouzounis C., Casari G., Schneider R., Sander C.,
Dolan M., Gilbert W., Gillevet P.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               267 AA; 30425 MW; D5912DD5B39A8451 CRC64;
                                                                                        Bacteria; Firmicutes; Mollicutes; Entomoplasmatales;
Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
1A protein [Includes: Helicase, Methyltransferase].
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Hypothetical protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               966 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z33006; CAA83689.1; -.
InterPro; IPR001454; Hlgnase/hydrlase.
InterPro; iPR001150; Hypothet_cof.
Pfan; PF00702; Hydrolase; 1.
PROSITE; PS01228; COF_1; 1.
PROSITE; PS01229; COF_2; 1.
PROSITE; PS01229; COF_2; 1.
Rypothetical protein.
NON TER.
SEQUENCE 267 AA; 30425 MW; D5912DD5B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=92074218; PubMed=1962437;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Broad bean mottle virus.
                                                                           Mycoplasma capricolum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     158 CFGKKENMRQMR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                    NCBI_TaxID=2095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Bawden;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bromovirus.
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1 MOLD SPECIAL STATES (1996).

1 FUNCTION: REGULATORY PHOTORECEPTOR WHICH EXISTS IN TWO FORMS THAT ARE REPRESENS.

2 ARE REPRESENSITY INTERCONVERTIBLE BY LIGHT: THE PRE FORM THAT ABSORBS MAXIMALLY IN THE RED REGION OF THE SPECTRUM AND THE PER FORM THAT ABSORBS MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN THOUSES MAXIMALLY IN THE FAR-RED REGION. PHOTOCONVERSION OF PR IN SECONVERSION OF PREAT OF CANACELS THE INDUCTION OF PR IN THE SEPRENSE. MARREAGE RECONVERSION OF PR IN THE SPECTRUM THE SMALL SHUBDING PROTEIN.

2C GENES INCLUDIANG THOSE ENCODING THE SMALL SHUBDING PROTEIN. PROTOCHLOROPHYLLIDE REDUCTASE, RRNA, ETC. IT ALSO CONTROLS. THE EXPRESSION OF A NUMBER OF WICHEAR BEPROSCHATE CARBOXYLASE, CRUAR, ETC. IT ALSO CONTROLS.

2C THE EXPRESSION OF ITS OWN GENES (S) IN A NEGATIVE FEEDBACK FASHION.

2C THE STREAMS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

2C THE SIMILARITY: CONTAINS ONE COVALENTLY LINKED TETRAPYRROLE CHROMOPHORE.

2C THE SIMILARITY: CONTAINS 2 PAS. (PER-ARMT-SIM) DIMERIZATION DOMAINS.

21 SIMILARITY: CONTAINS 1 HISTIDINE KINASE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=cv. Nipponbare;
Tahir M., Kanagae H., Takano M.,
Phytochrome C (PHYC) gene in rice: isolation and characterization of a complete coding sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae,
Ehrhartoldeae, Oryzeae, Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 275-378 FROM N.A.
MEDLINE-97019052; PubMed-8865668;
Mathews S., Sharrock R.A.,
"The phytochrome gene family in grasses (Poaceae): a phylogeny and evidence that grasses have a subset of the loci found in dicot
                                                                                                                                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                                                                                                                                   54.9%; Score 39; DB 1; Length 966; 53.3%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Indels
                                                                                                                                                                                                                                                                                                                                   966 AA; 109621 MW; DF592681D7231C8D CRC64;
                                                                                                                                                                                       PIR; A41699; P1BVBB.
InterPro; IPR002588; V methyltransf.
InterPro; IPR005666; Viral helicasel.
Pfam; PF01443; Viral helicasel; 1.
Pfam; PF01660; Vmethyltransf; 1.
Helicase; ATP-binding; Transferase.
NP_BIND
690
697
ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PHYC_ORYSA STANDARD; PRT; 1137 AA. 092W15; P93429; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 15-UUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     53.3%; Pred. N. five
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In) Plant Gene Register PGR98-210
                                                                                                                                                                     EMBL; M65138; AAA42740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347 CFKENKDWTENMRSV 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQ----WQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryza sativa (Rice).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             angiosperms."
                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription regulation; Photoreceptor; Phytochrome; Chromophore;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=MB4 / JCM 11007;
MEDLINE-1992386;
MEDLINE-1992816.
BAO Q., Tian Y. Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J.,
Chen Y., Xue Y., Lia X., Huang L., Dong X., Ma Y., Ling L.,
Tan H., Chen R., Wang J., Yu J., Yang H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .;
0
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Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
Thermoanaerobacteriaceae; Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           904 1124 HISTIDINE KINASE.
322 322 CHROMOPHORE (BY SIMILARITY).
272 279 F -> S (IN REF. 2).
292 292 C -> S (IN REF. 2).
1137 AA; 125982 MW; F2A520181CFE7B32 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Indels
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
25-JUN-2002 (Rel. 41, Last annotation update)
RPMB OR TIE1495.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 39;
3; Mismatches
                                                                                                                                                                                                   InterPro; IRR004359; HIS.KIN sig.
InterPro; IPR003661; His KinA.
InterPro; IPR001610; PAC.
InterPro; IPR001014; PAS. domain.
InterPro; IPR001014; PAS. domain.
InterPro; IPR001294; Phytochrome.
Pfam; PR00312; signal; 1.
Pfam; PR00318; PAS; 2.
Pfam; PR01590; GAF; 1.
Pfam; PR01590; GAF; 1.
PRINTS; PR01033; PHYTOCHROME.
SWART; SW00065; GAF; 1.
SWART; SW00084; HisRA; 1.
SWART; SW00086; PAC; 1.
SWART; SW00086; PAC; 1.
SWART; SW00086; PAC; 1.
SWART; SW00091; PAS; 2.
IGRRAMS; SW00091; PAS; 2.
                                                                                                                                                         EMBL, U61207; AAB41996.1; -.
InterPro; IPR003594; ATPbind ATPase.
InterPro; IPR003018; GAF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50109; HIS_KIN; 1.
PROSITE; PS5012; PAS; 2.
PROSITE; PS00245; PHYTOCHROME 1; 1.
PROSITE; PS50046; PHYTOCHROME 2; 1.
                                                                                                                                         EMBL; AB018442; BAA74448.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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Q8R9U1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
DOMAIN
BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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ProDom; PD000158;
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1113
1133
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1168
220
2210
267
42
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ACT_SITE
ACT_SITE
DISULFID
DISULFID
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                                                                                                                                                            CARBOHYD
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                                                                                                                                                  DISULFID
                                                        SIGNAL
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HUMAN
                                                                               CHAIN
                                                                                                                                                                                                                                                                Matches
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                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swies Institute of Bioinformatics and the EWBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                          ö
                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tisljar K., Deussing J., Peters C.; "cathepain J, anovel murine cysteine protease of the papain family with a placenta-restricted expression."; FBBS Lett. 459:299-304(1999).
                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                     -!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                           CATJ MOUSE STANDARD; PRT; 333 AA.
(9R014; Q9WV51;
16-OCT-2001 (Rel. 40, Last sequence update)
15-OCT-2001 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cathepsin J precursor (EC 3.4.22.-) (Cathepsin P) (Catlrp-p).
                                                                                                                                                                                 53.5%; Score 38; DB 1; Length 62; 60.0%; Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                          CAADB605C81D495D CRC64;
complete sequence of T. tengcongensis genome."; nome Res. 12:689-700(2002).
                                                                                                                                                                                                        3; Mismatches
                                                                                                                                    EMBL, AE013107, AAM24713.1; -.
Ribosomal protein, Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1349426; Ctsj.
InterPro; IPR000668; Peptidase Cl.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase Cl; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=99456833; Pubmed=10526153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF136272; AAF13142.1; -. EMBL; AF158182; AAD41898.1; -. HSSP; P07711; ICJL.
                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROPS; C01.038; -.
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                               QWQENMRKVR 12
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27 RWKPNIRKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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            Genome Res.
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P48163; Q16855; Q9BWX8; Q9UIY4; Q9H1W3;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Malic enzyme 1).
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Chou W.Y., Huang S.M., Chang G.G.;
"Nonidentity of the cDNA sequence of human breast cancer cell malic
enzyme to that from the normal human cell.";
J. Protein Chem. 15:273-279(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=94244767, PubMed=8187880;
Loeber G., Dworkin M.B., Infante A., Ahorn H.;
"Characterization of cytosolic malic enzyme in human tumor cells.";
FEBS Lett. 344:181-186(1994).
                                 PROSITE; PS00139; THIOL PROTEASE CYS; 1.
SROSITE; PS00639; THIOL PROTEASE TIS; 1.
PROSITE; PS00640; THIOL PROTEASE ASN; 1.
Hydrolase; Thiol protease; Glycoprotein; Lysosome; Zymogen; Signal.
                                                                                                                                                                                                                CATHEREN J.

BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
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-!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37147 MW; F9A8FF1D5A13B721 CRC64;
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-!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (IN REF. 2)
                                                                                                                                                                 POTENTIAL. ACTIVATION PEPTIDE
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Peptidase C1; 1.
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TISSUE=White adipose tissue;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 AA;
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51 WEENMRMIK 59
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us-09-743-107b-85.rsp

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TISSUE=Intestine;
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EMBL; M26589;
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EF2_CHICK
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JAN'-1990 (Rel. 13, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
MADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Malic enzyme 1).
MEI OR MODI OR MOD-1.
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Nikodem V.M.,
"Structural characterization of the rat malic enzyme gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:4912-4916(1989).
-!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2) +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Morioka H., Tennyson G.E., Nikodem V.M., "Structural and functional analysis of the rat malic enzyme gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nikodem V.M., Magnuson M.A., Dozin B., Morioka H.,
"Coding nucleotide sequence of rat malic enzyme mRNA and tissue specific regulation by thyroid hormone.";
Endoor. Res. 15:547-564 (1989).
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MEDLINE=86111756; PubMed=3753699;
Magnuson M.A., Morioka H., Tecce M.F., Nikodem V.M.;
"Coding nuclectide sequence of rat liver malic enzyme mRNA.";
J. Biol. Chem. 261:1183-1186(1986).
                                                                                                                                                                                                                                                                                                                                                                                     53.5%; Score 38; DB 1; Length 572; 33.3%; Pred. No. 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Indels
                                                                                                                                                                                                                                                                                                                         438 438 P -> S (IN REF. 2).
572 AA; 64149 MW; EA4C8CB36F6C619C CRC64;
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-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
                                                                                                                                                                                                                                                                                                     NADP (BY SIMILARITY).
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5; Mismatches
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  or send an email to license@isb-sib.ch)
                                                                                                                                                                                   InterPro; IPR001891; Malic_oxred.
Pfeam; PR00390; malic; 1.
PRINTS; PR00072; MALOXEDTASE.
PROSITE; PS00331; MALIC_ENZYMES; 1.
Oxidoreductase; NADP.
NP BIND 301 318 NADP (BY CONFLICT 438 P -> S (I
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MEDLINE=89296914; PubMed=2740332;
                                   EMBL; X77244; CAA54460.1; -.
EMBL; U43944; AAC50613.1; -.
EMBL; AL391416; CAC36330.1; -.
EMBL; AL136970; CAC19505.1; -.
EMBL; AL049699; CAB52344.1; -.
Genew; HGNC.6983; ME1.
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Matches 4, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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MEDLINE=91207327; PubMed=1708237;

Kim Y.W., Kim C.W., Kang K.R., Byun S.M., Kang Y.S.;

Kim T.W., Kim C.W., Rang K.R., Byun S.M., Kang Y.S.;

"Blongation factor-2 in chick embryo is phosphorylated on tyrosine as well as serine and threonine."; 4100-406 (1991).

Biochem Biophys. Res. Commun. 175:400-406 (1991).

- I- FUNCTION: THIS PROTEIN PROMOFIS THE GPP-DEPENNENT TRANSLOCATION OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PRINTS; PR00072; MALOXRDTASE.
PROSITE; PS00331; MALIC_ENZYMES; 1.
                                                                                                                                                                                                                                                                           EMBL, M26594; AAA41563.1; ALT SEQ.
EMBL, M26681; AAA41563.1; JOINED.
EMBL, M26682; AAA41563.1; JOINED.
EMBL; M26583; AAA41563.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, M26584, AAA41563.1, JOINED.
EMBL, M26585, AAA41563.1, JOINED.
EMBL, M26586, AAA41563.1, JOINED.
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EMBL; M26592; AAA41563.1; JOINED.
EMBL; M26593; AAA41563.1; JOINED.
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AAA41563.1; JOINED.
AAA41563.1; JOINED.
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InterPro; IPR001891; Malic_oxred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; NADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWQENMRKVR 12
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                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elongation factor; GTP-binding; Protein biosynthesis; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=88198187; PubMed=2834376;
Nakanishi T., Kohno K., Ishiura M., Ohashi H., Uchida T.;
"Complete nucleotide sequence and characterization of the 5'-flanking region of mammalian elongation factor 2 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 263:6384-6391(1988).
FINCTION: THIS PROTEIN PROMOTES THE GTP-DEPENDENT TRANSLOCATION OF THE NASCENT PROTEIN CHAIN FROM THE A-SITE TO THE P-SITE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                      -!- PTM: HIS-714 IS MODIFIED IN DIPHTAMIDE (2-[3-CARBOXYAMIDO-3-(TRIMETHYL-AMMONIO) PROPYL] HISTIDINE). DIPHTAMIDE CAN BE ADPRIBOSYLATED BY DIPHTERIA TOXIN AND BY PSEUDOMONAS EXOTOXIN A (BY
                                                                                                                                                                  SIMILARITY).
SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
EF-G/RF-2 SUBFAMILY.
                    -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- PTM: PHOSPHORYLATION BY EF-2 KINASE COMPLETELY INACTIVATES EF-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cricetulus griseus (Chinese hamster).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Cricetinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
6
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PHOSPHORYLATION (BY SIMILARITY)
PHOSPHORYLATION (BY SIMILARITY)
DIPHTRAMIDE (BY SIMILARITY).
3680187581F518E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 38; DB 1; Length 857;
Pred. No. 44;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
(BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MDR-1989 (Rel. 10, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           857 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR00640; BFG C.
InterPro; IPR004161; BFUT D2.
InterPro; IPR000795; BF GTPbind.
InterPro; IPR0005225; SWall GTP.
Pfam; PP00009; GTP_BFUT, 1.
Pfam; PF00679; BFG C; 1.
IGRFAMS; ILGR00231; SWall GTP; 1.
PROSITE; PS00301; BFATU D2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTP
GTP
GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95247 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U46663; AAA87587.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                      (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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P09445;
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NP_BIND
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R EMBL; JULZ.

R PIR; A26660; A280.

DR HSSP; P13551; 1FNM.

DR HSSP; P13551; 1FNM.

DR HIGEPPO; 1PR004161; EFTU D2.

DR InterPro; 1PR006405; EF GTPbind.

DR InterPro; 1PR006725; Small GTP.

DR Pfam; PF00609; GTP EFTU; 1.

DR Pfam; PF00115; EF00707; EFG C; 1.

DR PRINTS; PR00315; EF00707; EFTU D2; 1.

DR PRINTS; PR00315; EF00707; EFTU D2; 1.

DR PROSITE; PS00301; EFACTOR GTP; 1.

DR PROSITE; PS00301; EFACTOR GTP; 1.

TIGREAMS; TIGRO0231; Small GTP; 1.

DR PROSITE; PS00301; EFACTOR GTP; 1.

TWEAMS TIGRO021; Small GTP; 1.

DR PROSITE; PS00301; EFACTOR GTP; 1.

TO GTP (BY SIMILARITY).

TO GTP (BY SIMILARITY).
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                        -i- PTM: PHOSPHORYLATION BY BF-2 KINASE COMPLETELY INACTIVATES EF-2.
-i- PTM: HIS-714 IS MODIFIED IN DIPHTAMIDE (2-(3-CARBCXYAMIDO-3-(RINETHYL-AMMONIO)PROPYL]HISTIDINE). DIPHTAMIDE CAN BE ADP-RIBOSYLATED BY DIPHTAMIA TONIN AND BY PSEUDOMONAS EXOTOXIN A.
-i- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
SUBCELLULAR LOCATION: Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             682 FOWATKEGALCEENMRGVR 700
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                                                                                                                                                                                             EF-G/EF-2 SUBFAMILY.
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OM protein

Run on:

Sequence:

Searched:

Database

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P79722 brachydanio Ogybk9 drosophila Ogonzwo homo sapien Ogonzwa sariv Ogonzwa sariv Ogonzwa sariv Ogonzwa sariv Ogonzwa sariv Ogonzwa sarobacteri
                        Q97ti8 clostridium
Q96m21 homo sapien
Q8xse2 ralstonia s
Q9ewb1 streptomyce
Q9ewb4 streptomyce
                                                                                                                                                                                                      Q9bme7 aedes aegyp
Q95p39 aedes aegyp
Q8t4s0 aedes aegyp
Q8t4r9 aedes aegyp
Q9m7a9 oryza sativ
Q9m7a9 oryza sativ
                                                                                                                                                                                             Q945t7 hordeum vul
Q9vil8 drosophila
Q9xz30 drosophila
Q8sct3 pseudomonas
                                                                                                                                                           Q9xvdl caenorhabdi
Q9bnx0 unidentifie
                                                                                                                                                                             O9bnw0 peripatus s
O9bnw7 scolopendra
                                                                                                                                                                                                                                                                                                                                 Q8TCD2;
Q8TCD2;
Q8TCD2;
Q8TCD2;
Q8TCD2;
Q8TCD2;
Q8TCD2;
Q8TCD2 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Lactotransferrin.
Lactotransferrin.
Buco sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY_2000 (TrEMBLrel. 13, Created)
01-MAY_2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 61, DB 4; Length 711; Pred. No. 0.0091; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases. EMBL, BC022447, AAH22347.1; SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 AA.
                                                                                                                                                                                                                                                                                                                           711 AA
                                                                                                                                                                                                                                                                               ALIGNMENTS
                                          QBXSE2
Q9EWB1
Q9EWB4
                                                                    P79722
Q9VBK9
Q960C1
                                                                                                                                Q949E1
Q94937
Q8U788
Q9XVD1
Q9BNX0
Q9BNW0
                                                                                                                                                                                              Q945T7
Q9BME7
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Q8VWN1
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Q9NZW3
Q38115
Q96RS9
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Q8T4R9
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                 QBSCT3
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Local Similarity 90.9%;
les 10; Conservative (
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1 CFQWQENMRKV 11
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54.9
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Query Match
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Matches
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Q9UCY5
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090863 human immun
0908780 caenorhabdi
090az8 mus musculu
091zd5 mus musculu
091z75 mus musculu
082462 salmonella
097346 drosophila
087346 drosophila
087386 homo sapien
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O84824 chlamydia t
Q12124 saccharomyc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8tcd2 homo sapien
Q9ucy5 homo sapien
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29tr80 ovis aries
                                                                  (without alignments)
118.873 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                         February 21, 2003, 07:25:55; Search time 20.8 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                            671580
      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                         671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        - protein search, using sw model
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Q9DAZ8
Q91ZD5
Q91Z75
Q8Z462
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090863
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Q9UCY5
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Q8TAX2
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Q9NUS2
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sp_human:*
sp_invertebrate:*
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Bp_bacteriap:*
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                                                                                          US-09-743-107B-85
                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                              1 CFQWQENMRKVR 12
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sp_mhc:*
sp_organelle:
sp_phage:*
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sp_rodent:*
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Match Length DB
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Perfect score:
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Gaps

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Result Š.

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RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Rhite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Com L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

Bunn P., Etgu P., Feldhlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

RA Langin-Hooper S., Liu Z.A., Lucos J.S., Maiti R., Marziali A.,

RA Miltscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Bai G., Peterson J., Pham P.K., Rizzo M., Sonney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwatz J.R., Shinn P., Southwick A.M.,

Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,

Utterback T., Van Aken S., Vaysbergia V.S., Walker M.,

RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;

"Sequence and analysis of chromosome 1 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                 59.2%; Score 42; DB 10; Length 289; 58.3%; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                     Hypothetical protein.
SEQUENCE 289 Aa; 33338 MW; 753AA27BED0F840C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Coat protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein gp120 (Fragment).
                                                                                                                                                                                                                                                                         Nature 408:816-820(2000).
EMBL; AC079280; AAG50577.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            66.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1998 (TrEMBLrel, 08,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57.78;
                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 58.3
les 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWQENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                         8 CFTWEEYARHVR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=11676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 QWQENMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 EWKENLRKV 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=NJS182;
                                                                                                                                                                                                                                                            thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ghana."
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ID Q9
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                      "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
0
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 33;
                                                                                                                                                                                                            Score 57; DB 4; Length 38;
Pred. No. 0.0021;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                              InterPro, IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA; 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 17, Created)
(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70.4%; Score 50; DB 6; 63.6%; Pred. No. 0.035; ative 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana (Mouse-ear cress).
                                                                                                    seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995).
HSSP; P02788; IBKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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STRAIN-CV. COLUMBIA;
MEDLINE-21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
MEDLINE=95127729; PubMed=7827104;
                                        SEQUENCE FROM N.A.
MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, 077698; 1CB2.
InterPro, 1PR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-2001 (TrEMBLrel. 17, Lat
01-JUN-2001 (TrEMBLrel. 17, Lat
Hypothetical 33.3 kDa protein.
                                                                                                                                                                                                            80.3%;
                                                                                                                                                                                                                                         10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
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                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                    2 FQWQENMRKVR 12
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19 CYQWQKKMRKL 29
                                                                                                                                                                                                                                                                                                  21 FOWORNMRKVR 31
                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ovis aries (Sheep)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3702;
            NCBI_TaxID=9606;
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                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                             O9TR80;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41; DB 15; Length 81; Pred. No. 4.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases. EMBL; 4.228659; CAA.12841.1; -. InterPro; IRR000777; GP120. Pfan; PF00516; GP120; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 AA; 9138 MW; 2D43DCD554295572 CRC64;
01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                  Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
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POTENTIAL.
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MGD; MGI:1916256; 1600000123Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cathepsin-3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse)
                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                  4 WOENMRKVR 12
                                                                                                                                                                                                                                                                                                         52 WEENMKKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |:|||:|::
52 WEENMKKIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WOENMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cathepsin M.
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                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal.
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Q91ZD5;
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SEQUENCE TISSUE=PLACENTA;

MAISTINE=21085660, DubMed=11217851;

MA Azawa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

Azawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

MA Azawa K., Matsuda H.A., Ashburner M., Batalova S., Casavant T.,

MA Adota K., Matsuda H.A., Ashburner M., Batalova S., Casavant T.,

RA Adota K., Matsuda H.A., Ashburner M., Batalova S., Casavant T.,

MA Kuehl P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuehl P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J.,

Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,

Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

Brownstein M.J., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

K. Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

M. Lyons P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Saro K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

M. Wynshaw Boris B.A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wynshaw Boris B.A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

Dan Marchalla D., Wallen D., Mayanaw D.,

M. Wynshaw Boris B.A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

M. Wynshaw Boris B.A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                              Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                        "Genome sequence of the nematode C.elegans: A platform for investigating biology."; Science 282:2012-2018(1998). EMBL; Z81089; CAB03137.1; -. SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.7%; Score 41; DB 5; Length 275; 63.6%; Pred. No. 15; ive 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                       Submitted (OCT-1996) to the BMBL/GenBank/DDBJ databases
    01-FEB-1997 (TrEMBLrel. 02, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-07N-2001 (TrEMBLrel. 17, Created)
01-07N-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 AA.
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                                                                                                                                                                                                                                                                                                                 MEDLINE=99069613; PubMed=9851916;
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ses 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                           Caenorhabditis elegans.
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262 FQWKISMRKTR 272
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                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                    F53H4.4 protein.
                                                                                                                                                                     NCBI_TaxID=6239;
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Q9DAZ8

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS7BL/67; TISSUE=PLACENTA; Deussing J., Kouadio M., Rehman S., Werber I., Schwinde A., Peters C., "Identification and Characterization of a Dense Cluster of Placenta-specific Cysteine Peptidases and Related Genes on Mouse Chromosome
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                          57.7%; Score 41; DB 11; Length 332;
55.6%; Pred. No. 19;
ive 4; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR000668; Peptidase Cl.
InterPro; IPR000169; SHprot_acsite.
Pfam; PF00112; Peptidase Cl; 1.
PRINTS; PR00776; Papalu.
PRODOM; PD000158; Peptidase Cl; 1.
PROSITE; PS00639; THIOL PROTEASE HIS; UNKNOWN 1.
SEQUENCE 332 AA; 37298 MW; 0804FIBA5B6538E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 332 CATHEPSIN-3.
332 AA; 37326 MW; 4184B90725B41C0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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InterPro; IPR000668; Peptidase_C1.
InterPro; IPR001659; SHprot_acsite.
Pfan, PF00112; Peptidase_C1; 1.
ProDom; PD000158; Peptidase_C1; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
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NCBI_TaxID=7227;
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SEQUENCE
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Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davis R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmonella
enterica servor Typhi, CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                   57.7%; Score 41; DB 11; Length 333; 55.6%; Pred. No. 19; ive 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Indels
                  PERGENE FROM N.T. TISSUE-SPLEEN;
Rehman S., Peters C., Deussing J.;
Rubmitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AV657446; AAL15416.1;
InterPro; IPR000668; Peptidase Cl.
InterPro; IPR000169; SHprot_ac@ite.
Prom; PD00112; Peptidase Cl; 1.
Propon; PD000158; Peptidase Cl; 1.
PROSITE; PS00639; THIOL PROTEASE HIS; UNKNOWN 1.
SEQUENCE 333 AA; 37388 MM; 6DD0BEB91C0331I0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AL627276; CAD06049.1; -.
Hypothetical protein; Complete proteome.
SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                 01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sentence update)
Hypothetical protein STX3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
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V 58.3%; Pred. No. 30,
'... 0; Mismatches
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                                                                                                                                                                                                                                                                                  511 AA.
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CG11198 OR CG8723.
Drosophila melanogaster (Fruit fly).
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                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                   PRELIMINARY;
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Best Local Similarity
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 413:848-852
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
            SEQUENCE FROM N.A.
                                                                                                                                                                                                   4 WOENMRKVR 12
                                                                                                                                                                                                                        52 WEENMKKIK 60
                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhi
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                                                                                                                                                                                                                                                                                                                                                                                           Salmonella.
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09V346
AC 09V34
DT 01-MA
DT 01-MA
DT 01-MA
DT 01-MA
DE CG972
GN CG111
OS DFOSIO
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RAY Adams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Ray Adams N.D., Celniker S.E. in P.W., Hoskins R.A., Galle R.F., George R.A., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Kortman J.R., Yandell N.D., Zhang Q., Chen L.X., Sutton G.G., Wortman J.R., Yandell N.D., Zhang Q., Chen L.X., State B.D., Randon G.G., Wortman J.R., The H. G., Nelson C.R., Miklos G.L.G., Randwin D., Ballew R.M., Basu A., Barenal B.P., Bhandari D., Beasley E.M., Ballew R.M., Basu A., Barenal B.P., Bhandari D., Bolshakov S., Balcher R.C., Buten D.R., Denger D., Botchan M.R., Bouck U. Brotchan M.R., Bouck U. Brockedell D., Bolshakov S., Burchs K.C., Busam D.A., Deng Z., Mays A.D., Dew I., Diez Z. S.M., Berson K.Y., Long Z., Mays A.D., Dew I., Diez S. S.M., Re Pables B. D., Delcher A., Deng Z., Mays A.D., Dew I., Diez S.M., Achtery J.M., Cawley S., Dalloker B., Diedner M., Deng Z., Dunkov B.C., Dunn P., Dedorn K., Dowlor B.C., Perraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Gabriell J.H., Ravoy D., Heiman J.J., Hernandez J.R., Houck J., R.A., Hoult R.A., Hoult B. M., Marry D., Houston K.A., Hoult J.J., Harry D., Mosthrefi A., Mongre F., Gorrell J.H., We Z., Kennison J.A., Kechhum K.A., Mongre F., Gorrell J.H., Ke Z., Kennison J.A., Kechhum K.A., Boutte S., Kulp D., Lai Z., Liang Y., Lin X., Mattei B. W., Milahina N., Moly B., Murphy L., Muzny D.M., Nelson D.L., Rakinel B.E., Kodira C.D., Kraft C., Kravitz S., Mulp D., Lai Z., Shen H. G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y., Reene M. G., Shen R., Nelson B.K., Nelson R., Nelson B.K., Nelson R., Nelson B.K., Nelson R., Nelson B.K., Reinders R., Shen S., Pollard J., Pull J., Marg X., Shen B., Shen S.M., Woodage T., Worley K., Wang K., Shen S., Yeb, R., Weiner E.W., Yeh R.-F., Zaverl J.S., Zhan M., Zhang S., Zhu X., Shen H., Shill M., Zhaver J., Shon M., Zhang S., Yeh R., Zheng X.H., Wang Z., Zhu S., Zhang X.H., Wang Z., Zhu S., Wang Z., Zhu S., Wang Z., 
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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50.0%; Pred. No. 1.5e+02;
tive 2; Mismatches 4;
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Interpro; IPR000089; Biotin_lipoyl.
Interpro; IPR000082; Carboxyl_trans.
Interpro; IPR000901; CPSase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02(86; Biotin Carb C; 1. Pfam; PF03064; biotin lipoyl; 1. Pfam; PF001089; Carboxyl_trans; 1. Pfam; PF00289; CPSase L_Chain; 1. Pfam; PF02786; CPSase L_D2; 1. PR0SITE; PS001086; ENGTE, 1. PROSITE; PS00866; CPSASE_1; 1.
                                                                                                                                                                                                                                                    STRAIN=BERKELEY;
MEDLINE=20196006; PubMed=10731132;
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nes 6, Conservative
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                                                                                                                                                                                                           SECUENCE FROM N.A
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RESULT 12 Q8TAX2

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STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 70.0%; Pred. No. 35; 7; Conservative 0; Mismatches 3; Indels
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Andre B., Vissers S., Urrestarazu L.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urrestarazu L.A., Andre B., Vissers S.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murphy L., Richards C., Gentles S., Harris D.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Barrell B., Rajandream M.A.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398 AA; 44266 MW; 45B208AE61714A5E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UVN-2002 (TrEMBLrel. 21, Last annotation update)
Chromosome IV reading frame ORF YDL005C.
MED2 OR D2930 OR YDL005C.
                              rrrp 1 OR CT817.
Chlamydia trachomatis.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia trachomatis.";
Science 282:784-758(1998).
BMBL, AD00154; AAC68414.2;
InterPro: IPR002422; AAA/rel prmease2.
InterPro: IPR00201; ArAA permease.
Fam; PF03222; Trp Tyr perm; 1.
PRINTS; PR00166; AROAAPRNEASE.
TIGRFAMS; TIGR00837; araaP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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EMBL; Z48008; CAA88056.1; -.
EMBL; Z48432; CAA88354.1; -.
SGD; S0002163; MED2.
Tyrosine transport protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                        [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                             NCBI_TaxID=813;
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                                                                                                                                                                                                                                                                                                                                                                                                       Davis R.W.;
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AC 012124,
DT 01-NOV-11)
DE Chromoso
GN Saccharon
OC Saccharon
OC Saccharon
OC Succharon
OC
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Watenabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
Nakamura Y., Isogai T., Sugano S.;
Nakamura Y., Isogai T., Sugano S.;
Subnitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
Subnitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
InterPro; IPR00162; DnaJ.N.
FMBL; AKO0468; BAA91185.1.
FMART; SW06271; DnaJ.N.
FROSITE; PS5076; DnaJ. 1.
PROSITE; PS5076; DNAJ 2; 1.
PROSITE; PS5076; DNAJ 2; 1.
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                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jisoupherg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC025708; AAH25708.1; -.
Hypothetical protein.
SEQUENCE 306 AA; 34551 MW; 43D9AD722566B343 CRC64;
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                                                                                                                                                         01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to hypothetical protein FLJ11175.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
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01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                               306 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                               PRT;
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Best Local Similarity 55.6
Matches 5; Conservative
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Best Local Similarity 63.0,
7; Conservative
                                                                                        PRELIMINARY;
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TISSUE=PANCREAS;
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084824;
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RESULT 13 9EXN60

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RESULT 14

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                                                                        Query Match 56.3%; Score 40; DH 3; Length 431; Best Local Similarity 100.0%; Pred. No. 38; Matches 8; Conservative 0; Mismatches 0; Indels
KW Hypothetical protein.
SQ SEQUENCE 431 AA; 47717 MW; D3B0992B1F1A4892 CRC64;
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Oy 5 QENWRKVR 12 |||||||| Db 122 QENWRKVR 129

Search completed: February 21, 2003, 07:44:39 Job time: 21.8 secs

us-09-743-107b-86.rag

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February 21, 2003, 07:25:55; Search time 28.3 Seconds (without alignments) 56.502 Million cell updates/sec
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2: /SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
3: /SIDSZ/gcgdata/geneseqg-embl/AA1981.DAT:*
4: /SIDSZ/gcgdata/geneseqg-embl/AA1983.DAT:*
5: /SIDSZ/gcgdata/geneseqg-embl/AA1984.DAT:*
6: /SIDSZ/gcgdata/geneseqg/geneseqp-embl/AA1985.DAT:*
7: /SIDSZ/gcgdata/geneseqg/geneseqp-embl/AA1985.DAT:*
8: /SIDSZ/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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.: /SIDS2/gcgdata/
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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			Description		Human Lactorerrin	Human lactoferrin	Human lactoferrin	Himmy Income the	ייייייי דמרכיייייי	Human lactoferrin	Human lactoferrin	Himan Jactoferrin	Human Jactoferrin	Himan Jactoferrin	Human lactoferrin
SUMMARTES			ID		AA1/0000	AAY78038	AAY78046	AAY78047	10001244	AA1/803/	AAY78048	AAY78049	AAY78036	AAY78050	AAY78051
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AAR9855 AAY7803 AAY7806 AAY7806 AAY7806	AAY78065 AAY78034 AAY78034 AAY78067 AAK69352 AAW13397 AAY78033	AAY68867 AAY78032 AAR21810 AAR44841 AAR48530 AAR48531	AAR57462 AAR84699 AAR80263 AAR80264 AAR80264	AAW03045 AAR90607 AAR87622 AAR87622 AAW26150 AAW14036 AAW70310
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ALIGNMENTS

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Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                Baltzer L, Dolphin GT;
                                                                               Human lactoferrin derived peptide SEQ ID NO:86.
                  AAY78086 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                 98SE-0002441,
98SE-0002562,
98SE-0004614.
                                                                                                                                                                                                                              99WO-SE01230.
                                                           (first entry)
                                                                                                                                                                                                                                                                                          (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                     WO200001730-A1.
                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                             06-JUL-1999;
                                                                                                                                                                                                                                                  06-JUL-1998;
                                                                                                                                                                                                                                                            17-JUL-1998;
29-DEC-1998;
                                                           25-APR-2000
                                                                                                                                                                                                         13-JAN-2000.
                                                                                                                                                                Synthetic.
                                      AAY78086;
        RESULT 1
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Gaps

0;

Length 12;

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AAY78001 to AAY78100 represent peptides having sequences based on human
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Best Local Similarity 100.
Matches 12; Conservative
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29-DEC-1998;
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binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and or prevention of infections (act fragment can be used for treating and/or prevention of infections (ach as urinary tract infections, colitis, and candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula, anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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                                                                                                                                                                                                                                                                                                                                                                                                                       92.9%; Score 65; DB 21; Length 12 91.7%; Pred. No. 0.00018; ive 0; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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ses 11; Conservative
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29-DEC-1998;
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                                                                                                                                                      AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
                                                                                                                                                                                                                                                                                                                                                                                                        anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 70; DB 21; Length 12; 100.0%; Pred. No. 2.6e-05; ive 0; Mismatches 0; Indel8
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                                                                                                                  Claim 22; Page 36; 102pp; English
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98SE-0004614.
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12 AA;

Sequence

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as an anison be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canbe them to be used for the same purposes as lactoferrin at lower
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               Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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   may also be used as preservatives.
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                                                                                                                                                                                          Score 65; DB 21;
Pred. No. 0.00018;
0; Mismatches 1;
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 fungicidal and bactericidal and
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91.7%;
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98SE-0004614.
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Best Local Similarity 91.7
Matches 11; Conservative
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Synthetic.
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                              Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
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Score 65; DB 21; Length 12; Pred. No. 0.00018;
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                               1; Indels
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                                                                                                                                                                                                                                                                                    Human lactoferrin derived peptide SEQ ID NO:37.
                                 0; Mismatches
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98SE-0002562.
98SE-0004614.
92.9%;
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             Best Local Similarity 91.7
Matches 11, Conservative
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Matches 11; Conservative
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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                                                                                                                                                                        Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                                  Human lactoferrin derived peptide SEQ ID NO:49.
AAY78049 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 18; Page 74; 102pp; English.
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98SE-0004614.
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                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                     food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection, colitis, Candida infection, fungicidal, bactericidal, preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 0.0002;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                   Human lactoferrin derived peptide SEQ ID NO:48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 15; Page 74; 102pp; English
                                                                                                                                                          AAY78048 standard; Peptide; 13 AA
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Best Local Similarity 91.7
Matches 11, Conservative
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  12
                                         2 CFÓWORNMRKVR 13
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  CFOWOREMRKVR
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Baltzer L, Dolphin GT;

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0
                                            Gaps
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Query Match

92.9%; Score 65; DB 21; Length 13;

Best Local Similarity 91.7%; Pred. No. 0.0002;

Matches 11; Conservative 0; Mismatches 1: Indele
                                                                                                                                                                                                                                                                                                 Human lactoferrin derived peptide SEQ ID NO:36.
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RESULT 7

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us-09-743-107b-86.rag

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired
               Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Page 69; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                 Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                     98SE-0002441.
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29-DEC-1998;
                                                                                                        Homo sapiens
Synthetic.
                                                                                                                                                                                                                                     06-JUL-1999;
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 15; Page 75; 102pp; English.

Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;

WPI; 2000-147388/13.

98SE-0004614. 98SE-0002441. 98SE-0002562.

(ASCI-) A+ SCI INVEST AB

99WO-SE01230,

36-JUL-1999; 06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

13-JAN-2000

WO200001730-A1

Synthetic.

Gaps ó 92.9%; Score 65; DB 21; Length 14; 91.7%; Pred. No. 0.00021; ive 0; Mismatches 1; Indels 11; Conservative Query Match Best Local Similarity 14 AA; Seguence Matches à

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1 CFQWQREMRKVR 12

3 CFOWORNMRKVR 14

AAY78050 standard; Peptide; 14 AA. AAY78050; RESULT 9 AAX78050

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:50.

Human, lactoferrin, modification, infection, inflammation, tumour; food, infant formula, anti-inflammatory; anti-microbial, anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens

06-JUL-1999; 99WO-SE01230.

13-JAN-2000.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula and may also be used as preservatives.

Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and also the peptides as lactoferrin at lower and anti-tumbors. Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; Gaps 0; 92.9%; Score 65; DB 21; Length 14; 91.7%; Pred. No. 0.00021; live 0; Mismatches 1; Indels Human lactoferrin derived peptide SEQ ID NO:51. AAY78051 standard; Peptide; 14 AA. bactericidal; preservative 25-APR-2000 (first entry) 11; Conservative 1 CFOWOREMRKVR 12 14 Local Similarity 3 CFOWORNMRKVR 14 AA; WO200001730-A1. Homo sapiens. Synthetic Sequence AAY78051; Query Match cost. Matches RESULT 10 AAY78051 ð

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fundicial and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                                                                                                         anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                             New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      anti-ulcer agent; low toxicity; stable; heat-resistant.
                                                                                                     Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   - has low toxicity, is
                                                                                                     Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR98554 standard; Peptide; 15 AA.
                                                                                                                                                                                                          Claim 18; Page 75; 102pp; English.
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heat-resistant and water-soluble
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 11; 11pp; Japanese
                                                                                                     Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.9%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peptide for anti-ulcer agent,
                          98SE-0002562.
98SE-0004614.
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              98SE-0002441.
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Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 AA;
                            17-JUL-1998;
29-DEC-1998;
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            06-JUL-1998;
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                                                                                                     Hanson LA,
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AAR98554
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
            The agent is low oln.. It can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, lactoferrin, modification, infection, inflammation, tumour, food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection, fungicidal; bactericidal, preservative.
                                                                                                                                                    Gaps
                                                                                                                                                  0
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          AAR98531-54 are peptides used in an anti-ulcer agent. The a in toxicity, is heat-resistant and stable in aqueous soln.. administered orally and be produced in large amounts.
                                                                                                                  Length 15;
                                                                                                             Score 65; DB 17; Length 15
Pred, No. 0.00023;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                         AAY78035 standard; Peptide; 15 AA.
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98SE-0002562.
98SE-0004614.
                                                                                                             ch 92.9%;
.1 Similarity 91.7%;
11; Conservative
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                                                                                                                  Query Match
Best Local Similarity
                                                                                15 AA;
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29-DEC-1998;
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Matches
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15 AA;

Sequence

AAY78063 standard; Peptide; 15 AA.

RESULT 14 AAY78063

(first entry)

25-APR-2000

AAY78063;

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Even though native human lactoferrin have been shown to have desired
                                                                                                                                                                                                                                                                                                    Human, lactoferrin, modification, infection, inflammation, tumour,
food, infant formula; anti-inflammatory, anti-microbial, anti-tumour,
urinary tract infection, colitis, Candida infection, fungicidal;
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                                    Gaps
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Pred. No. 0.00023;
0; Mismatches 1; Indels
   DB 21; Length 15;
Score 65; DB 21; Length 15
Pred. No. 0.00023;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baltzer L, Dolphin GT;
                                                                                                                                                                                                                                                                         Human lactoferrin derived peptide SEQ ID NO:62.
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                                                                                                                                                                           AAY78062 standard; Peptide; 15 AA.
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 92.9%;
91.7%;
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98SE-0002562.
98SE-0004614.
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91.7%;
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                                                                                                                                                                                                                                                                                                                                                      bactericidal; preservative.
                                                                                                                                                                                                                                         (first entry)
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                                 Conservative
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Matches 11; Conservative
                                                             1 CPOWOREMRKVR 12
                                                                                           4 CPOWORNMRKVR 15
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               Local Similarity
Les 11; Conserv
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29-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
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 Query Match
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                              Matches
                                                                                                                                          RESULT 13
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                                                                                                             Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.9%; Score 65; DB 21; Length 15; 91.7%; Pred. No. 0.00023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dolphin GT;
                                                                               Human lactoferrin derived peptide SEQ ID NO:63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Page 81; 102pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY78031 standard; Peptide; 16 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                   99WO-SE01230.
                                                                                                                                                                                                                                                                                                                                                    98SE-0002441.
                                                                                                                                                                                                                                                                                                                                                                                   98SE-0004614.
                                                                                                                                                                                                                                                                                                                                                                     98SE-0002562,
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15 AA;
                                                                                                                                                                                                                                                 WO200001730-A1.
                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                   06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                    06-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                     17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                   29-DEC-1998;
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                                                                                                                                                                                                                   Synthetic.
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AAY78031
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AC AAY78
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0;

Gaps

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0; Mismatches

CFQWQREMRKVR 12 4 CFOWORNMRKVR 15

Matches

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the binding to specific lactoferrin receptors and are then transported through the directions classes and are then transported through the directions. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower capale them to be used for the same purposes as lactoferrin at lower
                                                                                 Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanson LA, Mattsby-Baltzer I, Baltzer L, Dolphin GT;
                                                  Human lactoferrin derived peptide SEQ ID NO:31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; Page 68; 102pp; English.
                 25-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                          WO200001730-A1.
                                                                                                                                                                                                                                                                                                                                                     06-JUL-1998;
17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                  06-JUL-1999;
                                                                                                                                                                                                                                                                               13-JAN-2000.
                                                                                                                                                                                                       Synthetic.
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98SE-0002441. 98SE-0002562. 98SE-0004614.

99WO-SE01230.

ö 0; Gaps Match 92.9%; Score 65; DB 21; Length 16; Local Similarity 91.7%; Pred. No. 0.00024; les 11; Conservative 0; Mismatches 1; Indels 1 CFOWOREMRKVR 12 16 AA; Query Match Matches ð

Search completed: February 21, 2003, 07:37:15 Job time : 28.35 secs

5 CFOWORNMRKVR 16

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Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 24, Appli
Sequence 24, Appli
Sequence 25, Appli
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Appli
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                                                               February 21, 2003, 07:25:59; Search time 8.65 Seconds (without alignments) 40.818 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25,
Sequence 4,
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1: /cgn2_6/ptodatca1/iaa/5A_COMB.pep:*
   /cgn2_6/ptodatca1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodatca1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodatca1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodatca1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodatca1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.3 (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-628-380-8

US-08-628-380-8

US-07-891-174-3

US-08-256-771-25

US-08-256-771-25

US-08-381-984-24

US-08-381-984-25

US-08-381-984-25

US-09-508-771-25

US-09-508-734-6

US-09-508-734-6

US-09-508-734-6

US-09-508-734-8

US-09-508-734-8

US-07-755-161A-8

US-07-755-161A-8

US-07-755-161A-8

US-07-755-161A-8

US-07-755-161A-8

US-07-755-161A-8

US-07-958-771-30

US-08-381-984-29

US-08-381-984-29
                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-406-271-5
                                                                                                                                                                                    262574 seqs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
                                                                                                                                                                Gapop 10.0 , Gapext 0.5
                                                                                                          US-09-743-107B-86
70
1 CFQWQREMRKVR 12
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query
Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
                                                                                                                                                     Scoring table:
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                                                                                                                                 Sequence:
                                                                                                                                                                                      Searched:
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                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                      US-U8-204-487-3
; Sequence 3, Application US/08204487
; Patent No. 5565425
; GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAVASHIMA, HIDEKI
APPLICANT: TANAKA, SHIGBAKI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: DOSAKO, SHUN'ICHI
APPLICANT: UCHIDA, TOSHIAKI
APPLICANT: TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURMITZ & ADDRESSEE: THIBBAULT
STREET: SA STATE STREET
CITY: BOSTON
STREET: MA
COUNTRY: USA
ZIP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER REALBLE FORDY disk
COMPUTER: Floppy disk
COMPUTER: INP PC COMPAtible
COMPUTER: INP PC COMPAtible
COMPANIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER:
FILING DATE: 02-MAR-1994
ATTONEY/AGENT INFORMATION:
NAWE: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REGISTRATION NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEQ 1D NO: 3:
SEQUENCE CHARACTERISTICS:
         US-08-406-271-2
US-08-724-586-2
US-08-471-586-2
US-09-932-190-2
US-08-655-640-4
US-08-655-640-4
US-08-655-640-4
US-08-154-019-4
US-08-461-333-4
US-08-461-333-4
US-08-76-793-4
US-08-76-793-4
US-08-76-793-4
US-08-76-793-7
US-08-76-793-7
US-08-75-703-2
US-08-75-703-2
US-08-75-703-2
US-08-75-703-2
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US-09-265-577-2
                                                                                                                                                                                                                                                                                                               ALIGNMENTS
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MEDIUM TYPE: Floppy
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STRANDEDNESS: si
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us-09-743-107b-86.rai

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internal
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Best Local Similarity
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US-08-628-380-8
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TELEX: 13
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                                           RESULT 3
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                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:

APPLICANT: YOUR MING LI
APPLICANT: HELEN VLASSARA
APPLICANT: HELEN VLASSARA
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                  ..
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                                                           Length 18;
                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                       Score 65; DB 1; I
Pred. No. 9.9e-05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 436
PRIOR APPLICATION DATA:
FILING DATE: UNNER: 08/488,217
FILING DATE: UNNER: 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7,1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
TELECOMMUNICATION 1NFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentr Pole
                                                                                                                                                                                                                                                                        Sequence 8, Application US/08485948
Patent No. 5855882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 Hackensack Avenue
OTHER INFORMATION: (20-37) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 201 343-1684
TELEK: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                       Query Match 92.9%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWOREMRKVR 12
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Best Local Similarity
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US-08-485-948-8
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US-08-204-487-3
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92.9%; Score 65; DB 1; Length 20;
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIPICATION 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                     PILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 3. SEQUENCE CHARACTERISTICS: LABNOTH: 20 amino acide TYPE: AMINO ACID STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOWE:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
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LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE:
CELL LINE:
ORGANELLE:
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STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-755-161A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Agent
TITLE OF INVENTION: Antimicrobial Agent
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 92.9%; Score 65; DB 2; I
Best Local Similarity 91.7%; Pred. No. 9.9e-05;
Matches 11; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE: 08/488,217
FILING DATE: 08/418,642
FILING DATE: 08/418,642
FILING DATE: 08/418,642
FILING DATE: APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7,1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 26,742
REPERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1879-5800
TELECAX: 201 343-1684
TELEFAX: 201 343-1684
TELEFAX: 201 343-1684
TELEFAX: SEQ ID NO: 8:
SEQUENCE CHARATERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-07-755-161A-3; Sequence 3, Application US/07755161A; Patent No. 5304633
                        ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JARAN--
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FRAGMENT TYPE: internal US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: single
      CORRESPONDENCE ADDRESS:
                                                                                        New Jersey
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWOREMRKVR 12
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                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                               07601
                                                                                                              COUNTRY:
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2" PUBLICATION INFORMATION: AUTHORS.
FEATURE:

NAME/KEST: modified site

LOCATION: 2

IDENTIFICATION METHOD:
OTHER INFORMATION: / hote= "thiol group of other information: / hote at location 2 connected by disulfide bond with OTHER INFORMATION: / thiol group of Cys residue at location 19"
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NAME/KEY: modified site
LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
AUTHORS.
AUTHORS.
      LOCATION: 2

IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
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APPLICANT: YAMAMOTO, NAOKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATREU
APPLICANT: TANAKA, SHICERALI
APPLICANT: TANAKA, SHICERALI
APPLICANT: TANAKA, YOSHIMIRO
APPLICANT: UNTHIDA, TOSHIMIRO
APPLICANT: UNTHIDA, TOSHIMIRO
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSE: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92.9%; Score 65; DB 1; Length 20; 91.7%; Pred. No. 0.00011; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY, AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REFIRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08204487
Patent No. 5565425
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                                                                                                                                                                                                             TITLE:
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                   VOLUME:
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Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                         Sequence 3, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUW TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDRESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-371-88:
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE:
                                                               1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
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CHROMOSOME/SEGMENT:
                                                                                                        2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 805 Fifte
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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UNITS:
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                                                                                                                                                                     RESULT 6
US-07-891-174-3
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US-08-256-771-24

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Patent No. 5656591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                 Query Match
92.9%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 0.00011;
Matches 11; Conservative 0; Mismatches 1; Indels
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OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                               LOCATION: 1.720
OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE
OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 805 Fifteenth Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24:
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 20 amino acids
TYPE: amino acid
                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                MOLECULE TYPE: peptide FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                         NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                           2 CPOWORNMRKVR 13
                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                TOPOLOGY:
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US-08-256-771-24
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Sequence 25, Application US/08256771

Patent No. 556591

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENITON: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENITON: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 fiteenth Street, N.W., #700
CITY: Mashington
                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.9%; Score 65; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 0.00011; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: INB Compatible
OCHUTER: INB COMPATIBLE
OCHUTER: Wardpertible
OCHUTER: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICE APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                            1 CFOWOREMRKVR 12
                                                                                                                   2 CFÓWORNMRKVR 13
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Query Match
Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
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US-08-381-984-24
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STATE:
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Sequence 1, 4. Application US/09508734

Sequence 4, Application US/09508734

Patent No. 6425509

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
USeful microorganism thereof
TITLE OF INVENTION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT PILING DATE: 1999-07-14

PRIOR PEPLICATION NUMBER: KR1998-29351

PRIOR FILING DATE: 1998-07-13

PRIOR APPLICATION NUMBER: KR1998-29351

NUMBER OF SEQ ID NOS: 12

SOFWWARE: Kopatentin 1.71

SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: /note= "the specified peptide as well as OTHER INFORMATION: peptides including the specified peptide as a fragment there
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                                                                                                                               MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/381,984 FILING DATE: APPLICATION NUMBER: US/08/381,984 FILING DATE: APPLICATION NUMBER: US/08/381,984
805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET UNMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Conservative
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                                                                                                                                                                                                                                                                                              CLASSIFICATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide FEATURE:
                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWQREMRKVR 12
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Best Local Similarity
Matches 11; Conserva
                          Washington
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                                                                    U.S.A.
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                                                                                             20005
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NAME/KEY:
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US-09-508-734-4
                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION
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OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 65; DB 1; Length 20; Pred. No. 0.00011; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: MS-DOS
SOFTWARE: MS-DOS
COMPUTER: April 11, 1995
CLASSIFICATION 252
PRICK APPLICATION DATA:
APPLICATION NUMBER:
                          Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fitteenth Street, N.W., #700
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-381-984-25
Sequence 25, Application US/08381984
Patent No. 5804555;
GRNERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
       Sequence 24, Application US/08381984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: 202-371-8850
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ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                                                                                                     STATE: D.C.
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NAME/KEY:
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FEATURE:
NAME/KEY: modified site
LOCATION: 21
LIDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified site
LOCATION: 4
LDENTIFICATION METHOD:
OTHER INFORMATION: //note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gape
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FILING DATE:
PRELEVATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                      ATTORNEY/AGENT INFORMATION:
NAME: WATEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFFAX: 202-371-8856
                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBLICATION INFORMATION: AUTHORS:
                                                                                                                                                                                                                                                                                        STRANDEDNESS: single
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
AVPOTHETICAL:
ANTI-SENSE:
FRACMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAP POSITION:
UNITS:
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US-09-508-734-6
; Sequence 6, Application US/09508734
; Patent No. 6423509
; GENERAL INFORMATION:
; APPLICANT: Sanyang Genex Corporation
; TITLE OF INVENTION: Useful microorganism thereof
; TITLE OF INVENTION: UNBER: US/09/508,734
; CURRENT FILING DATE: 1999-07-14
; PRIOR FILING DATE: 1999-07-14
; PRIOR FILING DATE: 1999-07-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 6
; LENGTH: 24
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                                                                                                                                                       0; Gaps
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                                                                                                         Score 65; DB 4; Length 22;
Pred. No. 0.00012;
0; Mismatches 1; Indels
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Pred. No. 0.00013;
0; Mismatches 1; Indels
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US-07-755-161A-10

J. Sequence 10, Application US/07755161A

Patent No. 5304633

GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent

TITLE OF INVENTION: Antimicrobial Agent

TITLE OF INVENTION: Antimicrobial Agent

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STATE: D.:

COUNTRY: U.S.A.

ZIP: Z0005

COMPUTER: Diskette, 5.25 inch, 500Kb

COMPUTER: Diskette, 5.25 inch, 500Kb

COMPUTER: DisplayWrite

COMPUTER: DisplayWrite

COMPUTER: DisplayWrite

CURRENT APPLICATION DATA:

ADDITION NATHORDER: IRANAINE
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91.7%;
                                                                                                     Query Match 92.9%;
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Conservative
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                TYPE: PRT
CORGANISM: Homo sapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                              1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                     2 CFOWORNMRKVR 13
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Best Local Similarity
Matches 11; Conserva
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LENGTH: 22
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FILING DATE
                                                                                                                 TITLE:
JOURNAL:
VOLUME:
                                                                                                                                                                             ISSUE:
                                                                                                                                                                                                    PAGES:
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                           Sequence 10, Application US/07891174
Patent No. 5317084
GREERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: I BM Compatible COMPUTER: I BM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: WAATEN M. Cheek JT.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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NAME/KEY: modified site
LOCATION: 21
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DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE TYPE:
CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                     US-07-891-174-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNITS:
FEATURE:
RESULT 15
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DENTIFICATION METHOD:

OTHER INFORMATION: (Date= "thiol group of other information 21 connected by disulfide bond with other information: (Tys residue at location 4" publication information: (Tys residue at location 4" admisors: Title: (The information information: (Tys residue at location 4" admisors: (Type: Title: (Type: Title: (Type: Type: Title: (Type: Type: Type: Type: (Type: Type: Type: Type: Type: Type: (Type: Type: Type:
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February 21, 2003, 07:51:54; Search time 10.5 Seconds (without alignments) 35.508 Million cell updates/sec
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i. cgn2_6/prodata/2/pubpaa/USOB NEW PUB.pep:*

i. cgn2_6/prodata/2/pubpaa/USOB NEW PUB.pep:*

i. cgn2_6/prodata/2/pubpaa/USOB NEW PUB.pep:*

i. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

i. cgn2_6/prodata/2/pubpaa/USO7_NEW PUB.pep:*

i. cgn2_6/prodata/2/pubpaa/USO7_NEW PUB.pep:*

i. cgn2_6/prodata/2/pubpaa/NEVOB_PUBCOMB.pep:*

i. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

i. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

i. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

ii. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

iii. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

iii. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

iii. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

iii. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

iii. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*

iii. cgn2_6/prodata/2/pubpaa/USOB_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      156504 seqs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Published Applications AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                 OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                             US-09-743-107B-86
                                                                                                                                                                                                                                                                                                                                                                                                          1 CFQWQREMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 5715, Appli Sequence 47,8E, A Sequence 48879, A Sequence 4, Appli Sequence 5, Appli Sequence 1340, Ap Sequence 20, Appli Sequence 2, Appli Sequence 3, Appli Sequence 3, Appli Sequence 23, Appli Sequence 22, Appli Sequence 22, Appli Sequence 2, Appli Sequence 2, Appli Sequence 29, Appli Sequence 29, Appli Sequence 2, Appli Description US-09-798-869-20 US-10-023-096-2 US-09-798-869-6 US-09-798-869-23 US-09-798-869-23 US-09-798-869-4 US-09-798-869-8 US-09-798-869-8 US-09-798-869-7 US-09-798-869-7 US-09-798-869-7 US-09-798-869-7 US-09-798-869-7 US-09-798-869-7 US-09-798-869-7 US-09-798-869-7 US-09-798-869-7 US-09-798-869-2 US-09-798-869-20 Length Query Match Score Result No.

US-09-864-761-47985 US-09-864-761-48879

US-09-867-550-1340

US-10-051-409-4 US-09-798-869-5

Sequence 9, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appl Sequence 15, Appl Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 24, Appli Sequence 1031, Appli Sequence 24, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 154, Appli Sequence 26, Appli		9; Length 15; . -05; Indels 0; Gaps 0;
10 US-09-904-536-8 10 US-09-904-536-11 10 US-09-904-536-11 10 US-09-904-536-12 10 US-09-904-536-13 10 US-09-904-536-14 10 US-09-904-536-16 10 US-09-904-536-16 10 US-09-904-536-16 10 US-09-904-536-16 10 US-09-904-536-10 10 US-09-904-536-10 10 US-09-904-536-10 10 US-09-904-536-10 10 US-09-904-536-10 10 US-09-904-536-10 10 US-09-904-536-10 10 US-09-913-806-6 10 US-09-913-806-6 10 US-09-138-626-5910 10 US-09-138-626-5910 10 US-09-138-626-5910 10 US-09-138-657-25 10 US-09-138-657-25 10 US-09-138-657-25 10 US-09-138-657-25 10 US-09-138-657-25 10 US-09-138-657-25 10 US-09-138-657-25 10 US-09-138-657-25 10 US-09-895-913A-154 10 US-09-895-913A-260 10 US-09-893-519A-64	ALIGNMENTS ion US/09798869 0030022821A1 URD SVENDSEN REMCAL STUTIBL (RNSSON BLOACTIVE PEPTIDES 1049-PCT-USA-A 11 2011-02-27 1 20011-02-27 1 20011-02-27 1 2001-02-27 1 2001-02-27 1 2001-02-27 1 2001-02-27 1 2001-02-27 1 2001-02-28 1 2001-02-28 1 2000-28 1 2000-31 1 299-08-38 1 30 0 ior Mindows Version 4.0	re 65; DB d. No. 6.6e Mismatches
335 335 335 335 335 335 335 335	2 No. US20 No. US20 No. US20 (YSTEIN TARENTION: LARS NOTE: A34 LICATION NOTE: B20 LD NOTE: B20 LD NOTE: B34 NOTE: B34 NOTE	ilarity Conservat Conservat NWRKVR 14 pplication . US200300 ATION: HN SIGNED ACSTEIN REM ALDUR SVEIN REM
01000000000000000000000000000000000000	RESULT 1 US-09-798-869- Sequence 2, PUBLICATION CAPPLICANT: APPLICANT: APPLIC	Query Match Best Local Sim Matches 11; Qy 1 CFOWQR Qy 2 CFOWQR CY 3 CFOWQR RESULT 2 US-09-798-869-20 Sequence 20, A Publicantion NO GENERAL INFORM APPLICANT: JO APPLICANT: JO APPLICANT: B

us-09-743-107b-86.rapb

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APPLICANT: Kurecki, Tomasz
APPLICANT: Kurecki, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell D.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin
                                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 9; Length 25; Pred. No. 0.00011; O; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1E: Jacobson, Price, Holman & Stern 400 Seventh St. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
         FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1050-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 10505/P58185C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
TELEPHONE: (202) 933-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION UNMBER: US 08/238,445
FILING DATE: 05-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-10-023-096-2
; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 92.9%;
91.7%;
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amino acid
                                                                                                                                                                                                                                                                                                                                                                                                            11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington D.C. COUNTRY: U.S.A. ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-10-023-096-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson,
LARS VORLAND
                                                                                                                                                                                                                                                                                                 CRGANISM: Homo Sapiens US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CFOWOREMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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                                                  Gaps
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Score 65; DB 9; Length 694;
Pred. No. 0.0025;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.4%; Score 57; DB 9; Length 15; 83.3%; Pred. No. 0.0014; Live 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                               | FULLICATION NO. USZUGJAUZZBZIAI |
| GENERAL INFORMATION: |
| APPLICANT: JOHN SIGGED SVENDSEN |
| APPLICANT: GYSTEIN REKDAL |
| APPLICANT: GYSTEIN REKDAL |
| APPLICANT: LARS VORLAND |
| TILLE OF INVENTION: BICACTIVE PEPTIDES |
| TILLE OF INVENTION: BICACTIVE PEPTIDES |
| FILE REFERENCE: AA404-PCT-USA-A |
| CURRENT APPLICATION NUMBER: US/09/798,869 |
| CURRENT PILLING DATE: 2001-02-21 |
| PRIOR PILLING DATE: 1999-08-31 |
| PRIOR PILLING DATE: 1999-08-28 |
| NUMBER OF SEQ ID NOS: 30 |
| SOFTWARE: FRASESQ for Windows Version 4.0 |
| SEQ ID NO 6 |
| LIBNGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09798869
Fublication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: USTEIN RENDAL
APPLICANT: GYSTEIN RENDAL
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: CG/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-36
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                 ; Sequence 6, Application US/09798869
; Publication No. US20030022821A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.18;
  Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                               1 CFQWQREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CFOWOREMRKVR 12
                                                                                                                                              22 CFOWORNMRKVR 33
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Matches 10; Conserva
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Best Local Similarity
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                                                                                                                                                                                                                                           9-698-867-60-SD
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US-09-798-869-3
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Query Match 71.4%; Score 50; DB 9; Length 25; Best Local Similarity 72.7%; Pred. No. 0.032; Matches 8; Conservative 1; Mismatches 2; Indels
                                                                                                                                 APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-36
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBU (RNSSON
APPLICANT: LARS VORLAND
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRSESQ FOR WINDOWS VERSION 4.0
                                                                            Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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ORGANISM: MURINE
                                   RESULT 8
US-09-798-869-22
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Gaps
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1; Indels
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gegreence 4, Application US/09798869
Fublication No. US20030022821A1
GENERAL INFORMATION
APPLICANT: USTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SEOTHARE: FASELSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: US/01-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SCOTTWARE: 23
LENGTH: 25
                                                                                                                                                                                Sequence 23, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: RYSTEIN REKCAL
APPLICANT: BALDUR SYBINBJ(RNSSON
APPLICANT: LARS VORLAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77.18;
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Matches 8; Conservative
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Best Local Similarity 72.7
Matches 8; Conservative
8; Conservative
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                                      1 CFQWQREMRKV 11
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                                                              3 CYQWQRRMRKL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: MURINE
                                                                                                                                             RESULT 6
US-09-798-869-23
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Matches
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OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine corner in other information: sequence)
US-09-798-869-8
                                                                                                                     Query Match 67.1%; Score 47; DB 9; Length 15; Best Local Similarity 72.7%; Pred. No. 0.062; Matches 8; Conservative 1; Mismatches 2; Indels
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ANDO. SEIKO
APPLICANT: HAYASHI, MIKIRO
APPLICANT: GOCHIAL, KEIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: YOKOI, HARUHIKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TATEISHI, NAOKO
APPLICANT: TREDA, MASATO
APPLICANT: IKEDA, MASATO
APPLICANT: SENOH, AKTHIRO
APPLICANT: OZAKI, AKIO
ITILE OF INVENITON: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 2000-04-07
PRIOR PILING DATE: 2000-08-03
NUMBER: OF EXQ ID NOS: 7059
SEQ ID NO 5715
LENGTH: 86
Sequence 30, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REXDAL
TITLE OF INVENTION: BLODRY SVEINBJ (RNSSON
TITLE OF INVENTION: BLODRY SVEINBJ (RNSSON
TITLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-26
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 30
INNERED: MINION SO 30
INNERE
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Publication No. US20020197605A1
GENERAL INFORMATION:
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ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 54.5
Matches 6; Conservative
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Matches 5; Conservative
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73 FEYRRQLRKIR 83
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; ORGANISM: BOVINE
US-09-798-869-30
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US-09-738-626-5715
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; ORGANISM: COLY;
US-09-738-626-5715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60.0%; Score 42; DB 9; Length 15; 54.5%; Pred. No. 0.41; Live 3; Mismatches 2; Indels
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Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: UOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKNAL
APPLICANT: LARS VORLAND
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOPTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                         APPLICANT: BALDUR SYBINAL

APPLICANT: BALDUR SYBINAL

APPLICANT: LARS VORLAND

TITLE OF INVENTION: BIOACTIVE PEPTIDES

CURRENT APPLICATION NUMBER: US/09/798,869

CURRENT FILING DATE: 2001-02-27

PRIOR APPLICATION NUMBER: ET/GB99/02851

PRIOR FILING DATE: 1999-08-31

PRIOR FILING DATE: 1998-08-38

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FASLSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 15
                                                                       Sequence 7, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURE SVENDSEN
APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 63.6
Matches 7; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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3 CYQWQWRMRKL 13
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US-09-798-869-29
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US-09-798-869-29
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US-09-798-869-30
          RESULT 10
US-09-798-869-7
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SEQ ID NO 29 LENGTH: 15 TYPE: PRT

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Search completed: February 21, 2003, 08:08:09 Job time : 10.55 secs
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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REPERBACE: Accomica X.-1

CURRENT PILLING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 99/632,366

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR FILING DATE: 2000-06-30

PRIOR PILLING DATE: 2000-06-30

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/0066

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR PRILING DATE: 2001-01-30

PRIOR PRILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR PRILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR PRILING DATE: 2001-01-30

PRIOR PRILING DATE: 2001-01-30
                     Sequence 2, Application US/09888320
Fublication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Berry III, Clifton E.
APPLICANT: DeBarber, Andrea E.
APPLICANT: Milul, Khisimuzi
APPLICANT: He Government of the United States of America
APPLICANT: as represented by The Secretary of the
APPLICANT: as represented by The Secretary of the
APPLICANT: Department of Health and Human Services
ITILE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFRENCE: 015280-413100US
CURRENT FILING DATE: 2001-06-22
FRIOR FILING DATE: 2000-06-26
FRIOR FILING DATE: 2000-06-26
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; OGGALISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-8888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
54.3%; Score 38; DB 9; Length 489;
Best Local Similarity 54.5%; Pred. No. 51;
Matches 6; Conservative 2; Mismatches 3; Indels
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APPLICATION NUMBER: PCT/US01/00668
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Patent No. US20020048763A1
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SEQ ID NO 2
LENGTH: 489
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US-09-864-761-47985
US-09-888-320-2
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Gaps
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, OTHER INFORMATION: MAP TO AL096701.14

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN HT474, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HTA74, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HTA7, SIGNAL = 1.6

10 OTHER INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUE 1.00e-06

US-09-864-761-47985
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PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 83.3
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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GenCore version 5.1.3
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sw model protein search, using protein ĕ Run on:

February 21, 2003, 07:25:55; Search time 9.6 Seconds (without alignments) 120.168 Million cell updates/sec

US-09-743-107B-86 70 1 CFQWQREMRKVR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 segs, 96134422 residues Searched: 283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

% Query Match Length DB ID	1	g !	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Description
.9 711		TFH	dī.	lactotransferrin p
7.1 708		JC2	323	lactoferrin - goat
.3 33 2		S 52	S52107	lactoferrin - shee
.4 707 1		A28	A28438	lactoferrin precur
.7 4568 2		TO	T08030	
.1 275 2		T2	T22597	hypothetical prote
.1 584 2		è	C84325	_
.1 932 2		12	T28820	hypothetical prote
.7 57 2		D8	D81949	
.7 376 2		36	S67085	_
.7 1266 2		AC	AC3154	conjugation protei
.7 1277 2		65	G98133	probable trak prot
121 2		AH	AH3147	hypothetical prote
.3 275 1		SO	S07442	interleukin-2 rece
.3 291 2		080	D86713	transcription regu
3 306 1		73	A39654	cell cycle arrest
.3 339 2		70	T09217	protein sam2B - sp
.3 489 2		C	C70655	probable monooxyge
.3 515 2		T0	T00510	probable cytochrom
4.3 536 2		12	T24218	hypothetical prote
4.3 543 2		Ē	T00513	cytochrome P450 ho
.3 572 1		DE	DERTMX	malate dehydrogena
.3 572 2		S4	S44415	malate dehydrogena
.3 638 2		$^{\rm s}$	S04640	methylmalonyl-CoA
4.3 979 2		Ţ	T08316	probable ATP-depen
4.3 4464 2		ă	D87755	protein T21E12.4 [
.9 206 2		Η	H97451	
2.9 206 2	Ţ,	AB	AB2670	ine
2.9		K	3441	

A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA, A;Residues: 20-31 <ST1>

A; Accession: S15853

A;Molecule type: protein A;Residues: 20-28,'X',30-31 <ST2>

A;Accession: S20841

A, Molecule type: mRNA A, Residues: 3-711 2000-5. A, Cross-references: EMBL:X52941; NID:934411; PIDN:CAA37116.1; PID:934412 R, Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W. Biochem. J. 276, 349-355, 1991 A, Title: Expression of cloned human lactoferrin in baby-hamster kidney cells. A, Reference number: S15853; MUID:91264786; PMID:2049066

A,Cross-references: GB.S52659; NID:g263311; PIDN:AAB24877.1; PID:g263312 A;Experimental source: placenta A;Experimental source: placenta Sylvote: sequence extracted from NCBI backbone (NCBIP:122202) B;Powell, M.J.; Ogden, J.E. Nucleic Acids Res. 18, 4013, 1990 A;Title: Nucleic de sequence of human lactoferrin cDNA. A;Reference number: \$10324; MUID:90326549; PMID:2374734 A;Accession: \$10324

hypothetical prote	interleukin-2 rece	MHC class I histoc	33.3K hypothetical	phytochrome C - so	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	probable dimethyla	hypothetical prote	hypothetical prote	serine/threonine k	probable tyrosine	hypothetical prote	conserved hypothet
H83682	JC1113	A45840	G86403	T14803	AG3273	C83633	AH2221	T47734	G71337	AD2346	S76885	B82921	C71467	T32605	AE0130
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37	37	'n	'n	m	m	1.1	` '	•			m			٠٠,	(*)

ALIGNMENTS

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A;Residues: 1-148, TT', 150-422, 'C', 424-711 <REY>
A;Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:934416
A;Cross-references: EMBL:X53961; NID:934415; PIDN:CAA37914.1; PID:934416
Mol. Endocrinol. 6, 1969-1981, N.; Malmer, D.; Panella, T.
A;Title: Differential molecular mechanism of the estrogen action that regulates lactofer: A;Reference number: A45401; MUID:93125571; PMID:1480183
                                                                              C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text_change 08-Dec-2000
C;Accession: G01394; S11228; Ā45401; S10324; S15853; S20841; S07160; A61169; A31000; S74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237 R;Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucleic Acida Res. 18, 5288, 1990 A;Title: Complete nucleotide sequence of human mammary gland lactoferrin. A;Reference number: S11228; MUID:90384839; PMID:2402455
                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-711 <CHO>
lactotransferrin precursor [validated] - human
                                                                                                                                                                                                            R;Cho, Y.
submitted to the EMBL Data Library, March 1994
Pareference number: G06820
A;Accession: G01394
                                               N;Alternate names: lactoferrin
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A; Residues: 1-15 <TEN>
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us-09-743-107b-86.rpr

DB 2;

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77.18;
72.78;
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Guest Iocal Similarity 63...
Best Iocal 7; Conservative
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                                                                                                                                               8; Conservative
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A; Residues: 3-707 <PEN>
                                                                                              Best Local Similarity
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A; Residues: 1-15 <LIU>
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A; Status: preliminary
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A; Residues: 436-487, 'A', 489-711 <RAD>
A; Cross-references: RMIS-MIS-642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R; Panella, T.J.; Liu, YI; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
A; Reference number: A61169; MUID:91235214; PMID:1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A Molecule type: protein

A, Molecule type: protein

A, Residues: 20-140,142-1169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4

A, Note: this is the final paper in a series

R; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

R; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

A; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

A; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

A; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

A; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

A; Reference number: S1, 30119; MUID:97054624; PMID:8898921
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F;1-19/Domain: signal sequence #status predicted <51G>
F;1-19/Domain: signal sequence #status predicted <51G>
F;20-711/Product: lactotransferrin #status experimental <MAT>
F;21-356/Domain: transferrin repeat homology <TRH1>
F;36-699/Domain: transferrin repeat homology <TRH2>
F;39-66,39-56,133-218,17-103,190-201,551-265,503-697,595-609/Disulfide bonds: #status efficience for the first of the first of
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R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-933, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of mR
A;Reference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 3-701,'SWXPVN' <PAN-
A; Experimental source: normal breast tissue
R; Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Bur, J. Blochen. 145, 659-666, 1984
A; Title: Human lactotransferzin: amino acid sequence and structural comparisons with oth
A; Reference number: A31000; MUID:85076667; PMID:6510420
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C;Dates: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Dates: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2223
B;Occession: OC2323; MulD:94380047; PMID:8093048
A;Acference number: JC2223; MulD:94380047; PMID:8093048
A;Acference number: JC2223; MulD:94380047; PMID:8093048
A;Accession: JC2223
A;Accession: JC2223
A;Accession: JC2223
C;Superfamily: transferrin; transferrin repeat homology
C;Superfamily: transferrin; plycoprotein
F;359-696/Domain: transferrin repeat homology
F;359-696/Domain: transferrin repeat homology
F;359-696/Domain: transferrin repeat homology
F;359-696/Domain: transferrin repeat homology (covalent) #status predicted
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C;Superfamily: transferrin; transferrin repeat homology
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A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
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C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: S52107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secretises takeference number: A92596; MUID:87280033; PMID:3611056
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J. Biol. Chem. 265, 21880-21885, 1991
A;fitle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: A208438; A41205
S;Pentecost, B.T.; Teng, C.T.
J. Biol. Chem. 262, 10134-10139. 1987
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                                                                  Gaps
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Length 708;
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A;Reaidues: 1-33 <QIA>
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:M74778
C;Superfamily: transferrin; transferrin repeat homology
C;Keywords: duplication; glycoprotein
   Score 54; DB 2;
Pred. No. 0.17;
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                                                                  2; Mismatches
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N,Alternate names: lactotransferrin
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Fing, W.V.; Kennedy, S.D.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, & J. Leitbauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablc Jung, K.H., Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Li A;Reference number: A84160; MUID:20504483; PMID:11016950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Introns: 14/2; 55/3; 86/2; 159/3; 220/2; 268/3; 327/1; 363/3; 402/3; 463/2; 559/3; 599
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A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis 22491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
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A;Experimental source: serogroup A, strain Z2491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein NMA1014 [imported] - Neisseria meningitidis (strain Z2491 serogroup
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A;Residues: 1-584 <STO>
A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
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A;Cross-references: EMBL:U50308; PIDN:AAC48001.1; GSPDB:GN00023; CESP:F07C3.1
A;Experimental source: strain Bristol N2; clone F07C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F07C3.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28820
R;Favello, A.; Gattung, S.
Submitted to the EMBL Data Library, March 1996
A;Description: The sequence of C. elegans cosmid F07C3.
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: D81949
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-57 <PAR>
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A;Gene: CESP:F07C3.1
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A;Gene: VNG1732C
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D81949
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                                                                                                             C; Species: Chlamydomonas reinhardtii
C; Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C; Accession. T08030
F; Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A; Titles. Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A; Reference number: 216302; MUID:94274778; PMID:8006077
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A,Introns: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3
C,Superfamily: dynein heavy chain, ciliary
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A, Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Adre: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
R;Dobson, R.
Submitted to the EMBL Data Library, October 1996
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C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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A;Molecule type: DNA
A;Residues: 1-4568 <MIT>
A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
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F;1919-1926/Region: nucleotide-binding motif A (P-loop)
F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                        dynein beta heavy chain - Chlamydomonas reinhardtii
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A, Status: preliminary, translated from GB/EMBL/DDBJ
A, Molecule type: DNA
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Pred. No. 18;
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50.0%;
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Best Local Similarity 63.6
Matches 7; Conservative
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1852 CFQWQSQLRYIQ 1863
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Best Local Similarity
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A,Introns: 67/1; 153/1
C,Superfamil:
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Conservative

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Matches

Query Match Best Local Similarity

A; Gene: NMA1014

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R; Weinberg, N. D.; Shaw, J.; Paetkau, V.; Bleackley, R.C.; Magnuson, N.S.; Reeves, R.; M. Immunology 63, 603-610, 1988
A; Title: Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen).
A; Reference number: S07442; MUID:88212503; PMID:2835311
C; Species: Agrobacterium timefaciens (strain C58, Cereon) C; Species: Agrobacterium timefaciens (c; Species: Agrobacterium timefaciens (c; Species: Agrobacterium timefaciens (c; Species: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 11-Jan-2002 (Jacession: G98133 R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B. Science 294, 2332-2328, 2001 Rathogen and Biotechnology Agent Agrobacterium tu A; Reference number: A97359; PMID:11743194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein Atu4804 (imported) - Agrobacterium tumefaciens (strain C58, Dupont C,Species: Agrobacterium tumefaciens C,Species: Agrobacterium tumefaciens C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
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R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,
R; Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ster, E.W.
A,Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A,Reference number: AB2577; PMID:11743193
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-121 <KUR>
A;Cross-references: GB:AE008689; PIDN:AAL45598.1; PID:g17743317; GSPDB:GN00187
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: GB: AE007870; PIDN: AAK88593.1; PID: g15158306; GSPDB: GN00170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55.7%; Score 39; DB 2; Length 127
77.8%; Pred. No. 1.2e+02;
tive 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: Atu4804
A;Map position: linear chromosome
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Best Local Similarity
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14 CLAWQRRNRRV 24
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A, Molecule type: DNA
A, Residues: 1-1277 < KUR>
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Science 294, 2317-2323, 2001
A;Authorg: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Cross-references: EMBL:Z75101; NID:g1431575; PID:e252673; PID:g1431578; GSPDB:GN00015; A,Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58. A;Reference number: AB2577; PMID:11743193 A;Accession: AC3154
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C,Species: Agrobacterium tumefaciens
C,Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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A,Molecule type: DNA
A,Rebidues: 1-1266 «KUR»
A,Cosb.references: GB:AE008689; PIDN:AAL45649.1; PID:g17743373; GSPDB:GN00187
A,Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein YOR193w - yeast (Saccharomyces cerevisiae)
NyAlternate names: hypothetical protein 04797
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 19-Apr-2002
C;Accession: S67085
R;Hughes, B.; Pohl, T.M.
submitted to the Protein Sequence Database, July 1996
A;Reference number: S66685
A;Reference number: S66685
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Pred. No. 36;
3; Mismatches 1; Indels
                                                 55.7%; Score 39; DB 2; Length 57; 66.7%; Pred. No. 5.7; tive 1; Mismatches 3; Indels
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55.7%;

Query Match Best Local Similarity 60.0. The 6; Conservative

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RESULT 11

C, Accession: AC3154

A,Gene: MIPS:YOR193w A,Cross-references: SGD:S0005719 A,Map position: 15R

C;Genetics:

A; Molecule type: DNA A; Residues: 1-376 < HUG>

A, Map position: linear chromosome

Query Match
Beet Local Similarity
7; Conserve

1142 ÓWÓŘĚQŘDV 1150

셤

3 QWQREMRKV 11

A; Accession: S07442

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A; Crosplex: 1-2, 5 cMal.)
A; Crosplex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains C; Complex: The high affinity receptor is a heterotrimer of alpha, beta, and gamma chains f; Function:
A; Penchion:
A; Pethway: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK C; Superfamily: interleukin-2 stimulated growth and differentiation of T cells, B cells, NK C; Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology C; Superfamily: interleukin-2 receptor alpha chain; complement factor H repeat homology cells.
F; 22-275/Product: interleukin-2 receptor alpha chain #status predicted cells.
F; 22-275/Product: interleukin-2 receptor alpha chain #status predicted cells.
F; 24-477/Domain: extracellular #status predicted cells.
F; 24-454/Domain: complement factor H repeat homology cells.
F; 24-454/Domain: transmembrane #status predicted cilm;
F; 265-275/Domain: intracellular #
                                                                                                                                                                                                                   A; Residues: 1-275 <WEI>
A; Status: preliminary A; Molecule type: mRNA
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261 CLIWQRKWKKNR 272 1 CFOWOREMRKVR 12 δ q

6; Conservative

Matches

Local Similarity

Query Match

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Gaps

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54.3%; Score 38; DB 1; Length 275; 50.0%; Pred. No. 40; tive 2; Mismatches 4; Indels

transcription regulator [imported] - Lactococcus lactis subsp. lactis (strain IL1403) C;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001

C, Accession: D86713
(C, Bancker, P., Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrli
(C, Bancher, C, A) (C, A)

A; Accession: D86713

A;Status: preliminary
A;Atacus: prep; DNA
A;Modecule type: DNA
A;Residues: 1-291 <STO>
A;Cross-references: GB:AE005176; PID:g12723619; PIDN:AAK04806.1; GSPDB:GN00146
A;Experimental source: strain IL1403
C;Genetics:
A;Gene: rmaB

0; Gaps 54.3%; Score 38; DB 2; Length 291; 85.7%; Pred. No. 42; 1; Mismatches 0; Indels Conservative Local Similarity Query Match Best Loca Matches

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4 WOREMRK 10

189 WOREMRR 195

Search completed: February 21, 2003, 07:47:58 Job time : 10.65 secs

Page 1

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GenCore version 5.1.3
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OM protein - protein search, using sw model

February 21, 2003, 07:25:55 ; Search time 4.6 Seconds (without alignments) 108.199 Million cell updates/sec Run on:

US-09-743-107B-86 70 1 CFQWQREMRKVR 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARIES

	Description	P02788 homo sapien	_	Q29477 capra hircu	_	Q39565 chlamydomon			Q9xz18 drosophila	3 sacch	P48163 homo sapien	7 rattu	P11652 propionibac		Q19020 caenorhabdi	P26898 ovis aries	Q15031 homo sapien	P93528 sorghum bic		Q9cg20 lactococcus	P06801 mus musculu			O28816 archaeoglob				Q20351 caenorhabdi			3	_	60	Q9ute7 schizosacch
SUMMARIES	ID	TRFL HUMAN	TRFL CAMDR	TRFL CAPHI	TRFL MOUSE	DYHB_CHLRE	TRFL HORSE	IL2A BOVIN	NLA DROME	BUB2_YEAST	MAOX HUMAN	MAOX_RAT	MUTA_PROFR	YNR2_CAEEL	DYHC CAEEL	IL2A SHEEP	SYLM HUMAN	PHYC_SORBI	RPOB_LIBAF	DCE_LACLA	MAOX MOUSE	Y008_HUMAN	T2D2_DROME	YES6_ARCFU	PMRD_SALTY	FL3L_HUMAN		TPSB_CAEEL		1	ARLY_AQUAE		- 1	MSS1_SCHPO
	Length DB	711 1	708 1													275 1																		496 1
de	Query	92.9	77.1	77.1	71.4	n	7		54.3	54.3	54.3	54.3	54.3	54.3	54.3	52.9	52.9	52.9	51.4	51.4	51.4	51.4	51.4	20.0	20.0	50.0	50.0	50.0	50.0	50.0	50.0	50.0	20.0	50.0
	Score	65	54	54	50	46	40	38	38	38	38	38	38	38	38	37	37	37	36	36	36	36	36	35	32	35	35	35	35	35	35	35	32	35
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Q9fg65 arabidopsis Q9um07 homo sapien	P14632 sus scrofa 077698 bubalus bub	035274 rattus norv	Q10201 schizosacch	Q9zwi9 oryza sativ	Q01371 neurospora	P30155 nicotiana t	P57070 vibrio chol	P18132 cryptococcu
C911_ARATH PDIS_HUMAN	TRFL_PIG TRFL_BUBBU	NEB2_RAT	YBX7_SCHPO	PHYC ORYSA	WC1_NEUCR	RK27 TOBAC	LOLB VIBCH	PYRE_CRYNE
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502	704	817	962	1137	1167	179	211	225
50.0	50.0	50.0	20.0	20.0	20.0	48.6	48.6	48.6
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34 35	36	38	v 4 v 0	41	42	43	44	45

ALIGNMENTS

RESULT	LT 1
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A P	O16786; O16789; C
AC	
Τď	(Rel. 01,
Ы	Last
Į	(Rel. 41, Last annotation update)
E	precursor
DE	Lactoferroxin B; Lactoferroxin C].
Z S	LITE OR LF.
SO	
ဥ္ပင္မ	Metazoa; Chordata; Cranlata; Vertebrata;
ဗ	1a;
ŏ	NCBI_TaxID=9606;
K.	
χ. Υ. Ι	SEQUENCE FROM N.A.
E E	TISSUE-Mammary gland;
2:	
\$ F	Pleper F.R.;
Y C	"Complete nucleotide Sequence or numan mammary gland lactorerrin."; Nucleic Acids Dec 10.6700.5700(1000)
2 2	131 MULTELL ACTUS RES. 18:3200(1730).
00	LA MODE GONDAN N N
4 6	FROM IN
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2 ;	
Z E	Inesis (1994), Genetic Engineering Research Institute / Taejon, Korea.
N E	[3]
¥ ;	SEQUENCE FROM N.A.
RA	Conneely O.M.;
Z.	Submitted (MAY-1992) to the EMBL/GenBank/DDBJ databases.
N.	[4]
RP	SEQUENCE FROM N.A.
RC I	TISSUB=Mammary gland;
RA	T
$\mathbf{R}\mathbf{I}$	nd sequence analysis of hu
RI	Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
RN	[5]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Bone marrow;
K.	Wei X., Han J., Rado T.A.;
RT	"Human neutrophil lactoferrin coding and 5' flanking region DNA
RT	368.";
RL	Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
Z.	
RP	SECUENCE FROM N.A.
RC	TISSUE=Mammarv gland:
8	Cheng H., Chen X., Huan L.;
RT	"CDNA cloning and sequence analysis of human lactoferrin.";
Æ	EMBL/GenBank/DDBJ databases.
RN	
RP	SEQUENCE FROM N.A.
RC	TISSUE=Prostate;
R.A	
RL	mitted
RN	[8]

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Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.;
                           awamori
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EMBL;
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of
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MEDLINE-82046817; PubMed-6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
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Nicholson H., Anderson B.F., Bland T., Shewry S.C., Tweedie J.W.,
                                                                                                                                                                                                                                      "The present state of the human lactotransferrin sequence. Study alignment of the cyanogen bromide fragments and characterization N- and C-terminal domains.";
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MEDLINE=88001031; PubMed=3477300;
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"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
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                                                                                                             Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haridas M., Anderson B.F., Baker E.N.;
"Structure of human diferric lactoferrin refined at 2.2-A
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MEDLINE=99190892; PubMed=10089347;
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                                                                                                                                                   comparisons with other transferrins.";
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MEDLINE=85076667; PubMed=6510420;
           TISSUE=Mammary gland;
mbDLINR=2022649; PubMed=2374734;
Powell M.1, Ogden J.E.;
"Nucleotide sequence of human laci
                                                                                                                                                                                                                                                                                                                 MEDLINE=82262043; PubMed=7049727;
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FEBS Lett. 142:107-110(1982).
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Rintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,

Rintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N.,

Rugar J., Kumaramanickavel G., Munier F., Schorderet D.F.,

But Matri L., Iwata F., Kaiser-Kupier M., Nagata M., Nakayau K.,

B. Hattin ancik J.F., Teng C.T.;

Hejtmancik J.F., Teng C.T.;

Hejtmancik J.F., Teng C.T.;

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CAN BIND TWO ATOMS OF FERRIC IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUBLIX BICARBONATE.

-- FUNCTION: LACTOFERROXINS A, B AND C HAVE CPICID ANTAGONIST

ACTIVITY: LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPTORS, WHILE LACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE

C. - FUNCTION: CAN C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE

C. - FUNCTION: CAN C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE

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C. - FUNCTION: CAN C HAVE DEGREPTORS.
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE=91166929; PubMed=1369293;
Tani F., Iio K., Chiba H. Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
'Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                              Jameson G.B., Anderson B.F., Norris G.E., Thomas D.H., Baker B.N., Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change."; Acta Crystallogr. D 54:1319-1335 (1998).
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-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=99192677; PubMed=10089508;
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                                                                                Acta Crystallogr. D 55:403-407(1999).
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M83205; AAA58656.1; -.
M18642; AAA86665.1; -.
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PubMed=9873069;
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31-OCT-93.
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1LFH;
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1HSE;
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TISSUE-Mammary gland;
MEDLINE-94380047; PubMed=8093048;
MEDLINE-94380047; PubMed=8093048;
le Provost F., Nocart M., Guerin G., Martin P.;
"Characterization of the goat lactoferrin cDNA. Assignment of the relevant locus to bovine Ul2 synteny group.";
Blochem. Blophys. Res. Commun. 203:1324-1332(1994).
-: FUNCTION: TRANSFERRING ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
-: SUBUNIT: MONOMER (BY SIMILARITY).
-: SUBCHLULAR LOCATION: Secreted.
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Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Capra.
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G -> A (IN REF. 2).
G -> P (IN REF. 2).
LLS -> PLF (IN REF. 2).
L -> F (IN REF. 2).
A -> P (IN REF. 2).
W; 0BOCLT5A0B69D430 CRC64;
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Lee T., Yu S., Kim S., Lee K., Yu D.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                  IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
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N-LINKED (GLCNAC.
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Best Local Similarity
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Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (JUN-1999) to the EMBL/GenBanik/DDBJ databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                           Gaps
                                                                                                                                                                                                                                                                                  Camelus dromedarius (Dromedary) (Arabian camel),
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Camelus.
                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Somali; TISSUB=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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INTERPOST IPROUIDS6; Transferrin.
Pfam; PF00402; Transferrin, 2.
PRINTS; PR00402; TRANSFERRIN.
PROSTER; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN. 1; 2.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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           92.9%; Score 65; DB 1; Length 711; ilarity 91.7%; Pred, No. 0.00066; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                         TRFL CAMDR STANDARD; PRT; 708 AA. 09TUNO; Q9MZS5; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-0T-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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EMBL; AF165879; AAF82241.1; -.
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Pfam, PF00405, transferrin, 2.

PRINTS, PR00402, TRANSFERRIN.

SMARY, SM00094, TR FER, 2.

PROSITE; PS00205, TRANSFERRIN 1; 2.

PROSITE; PS00206, TRANSFERRIN 2; 2.

PROSITE; PS00207, TRANSFERRIN 3; 2.

Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
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-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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Q -> K (IN REF. 2).
F -> P (IN REF. 2).
S -> R (IN REF. 2).
D -> G (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-14 FROM N.A. MEDILIBE-20240909; PubMed=1939212; MEDILIBE-20240909; PubMed=1939212; Liu Y., Teng C.T.; "Characterization of estrogen-responsive mouse lactoferrin promoter."; "Characterization of estrogen-responsive mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol, Chem. 266:21880-21885(1991)
-1- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pentecost B.T., Teng C.T.; "Lactotransferin is the major estrogen inducible protein of mouse
                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfan, PF00405; transferrin; 2.
PRINTS, PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN. 1; 1.
PROSITE; PS00206; TRANSFERRIN. 2; 2.
PROSITE; PS00207; TRANSFERRIN. 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Uterus;
Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
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Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases
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-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- DOMAIN: COMPOSED TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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LACTOTRANSFERRIN.
TRFL MOUSE STANDARD; PRT; 707 AA. P08071; P70690; Q61799; Q922P2; 01-AUG-1988 (Rel. 08, Created) 15-UN-2002 (Rel. 41, Last sequence update) 15-UN-2002 (Rel. 41, Last sequence update) Lactotransferrin precursor (Lactoferrin).
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J. Biol. Chem. 262:10134-10139(1987)
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EMBL; D885.0; BAA13633.1; --
EMBL; BC066994; AAA68904.1; --
EMBL; M74778; AAA39427.1; --
PIR; A28438; A28438.
HSSP; P02788; LCE.
MGD; MGL:96897; Ltf.
InterPro; IPR001156; Transferrin.
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MEDLINE=87280033; PubMed=3611056;
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J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND
FLAGELIA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mitchell D.R., Brown K.S.; "Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DYNEIN HAS ATPASE ACTIVITY.
SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND
GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
                                                                                                                                                                                                           ANION (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
MR -> 1QG (IN REF. 1).
R -> Q (IN REF. 2).
M -> L (IN REF. 2).
S -> T (IN REF. 2).
S -> T (IN REF. 2).
E -> G (IN REF. 2).
L -> V (IN REF. 2).
L -> V (IN REF. 1).
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Eukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales;
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IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
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01-NOV-1997 (Rel. 35, Last sequence update)
30-NAY-2000 (Rel. 39, Last annotation update)
OMPHEN beta chain, flagellar outer arm.
ODA4 OR ODA-4 OR SUP1.
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NCBI_TaxID=3055;
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MEDLINE=94274778; PubMed=8006077;
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-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
-!- SUBUNIT: MONOMER.
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P. "Three-dimensional structure of mare diferric lactoferrin at 2.6-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Jugues variatus "Netresca; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Equidae; Equus.
Mammalia; Eutheria; Perissodactyla; Equidae; Equus
                                                                                                                                                                                                                                                                                                                                                 COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                  EMBL; U02963; AAA19956.1; -.
Interpro; IPR04273; Dynein, heavy.
Pfan; PP03028; Dynein, heavy; 1.
Motor proțein; Microtubules; Dynein; ATP-binding; Flagella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 4568;
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9A9A5393C7C36AE7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "cDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COLLED COLL (POTENTIAL)
COLLED COLL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATP (POTENTIAL)
ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL) (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65.7%; Score 46; DB 50.0%; Pred. No. 9.4; tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                   COILED COIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Milk;
MEDLINE=99296631; PubMed=10366507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA; 519961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lactotransferrin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                 1650
1825
2045
2045
3162
3425
3425
3728
11926
22209
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1852 CFQWQSQLRYIQ 1863
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9796;
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3339
3648
1919
2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2530
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15-JUN-2002
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NP_BIND
NP_BIND
NP_BIND
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL). (POTENTIAL). (POTENTIAL).
                                                                                                   PDB; 1B1X; 02-PEG-98.
PDB; 1B1X; 02-PEB-99.
PROFITE; PRO01156; Transferrin; 2.
PRINTS; PRO0405; TRANSFERRIN.
SMART; SMO0094; TR FER; 2.
PROSITE; PS00206; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 1.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 40; DB 1; Length 695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07BB84D50E1B165D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (P
                                                                                                                                                                                                                                                      LACTOTRANSFERRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   275 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | IL2A_BOVIN
| IL2A_BOVIN STANDARD;
| AC | PL2342;
| DT 01-OCT-1989 (Rel. 12, Created)
                                                                                              EMBL; AJ010930; CAA09407.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.1%;
58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7; Conservative
                                                                                                                                                                                                                                                                                                                    179
189
187
251
251
386
377
690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                           351
15
25
121
163
166
176
237
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4631
5579
6311
663
663
663
664
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685
559
559
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DISULFID
DISULFID
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CARBOHYD
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SIGNAL
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0
                                                                                                                                                                                                          MEDLINE-88212503; PubMed=2835311; MeInberg A.D., Shaw J., Paetkau V., Bleackley R.C., Magnuson N.S., Reeves R., Magnuson D.A., Reeves R., Magnuson D.A., "Cloning of cDNA for the bovine IL-2 receptor (bovine Tac antigen)."; Immunology 63:603-610(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                  Bos taurus (Bovine).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N'LINKED (GLCNAC. . .) (POTENTIAL).
N'LINKED (GLCNAC. . .) (POTENTIAL).
W, 4901BBP9A4862390 CRC64;
01-OCT-1989 (Rel. 12, Last sequence update)
LeCCT-2001 (Rel. 40, Last annotation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERLEUKIN-2 RECEPTOR ALPHA CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Receptor; Repeat; Signal; Sushi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 38; DB 1; Length 275;
Pred. No. 13;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUSHI 1.
SUSHI 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M20818; AAA51414.1; -...
EMBL; U42226; AAC48487.1; -...
HSP; S07442; S07442.
HSSP; P01589; IIIM.
InterPro; IFRO04456; Sushi_SCR_CCP.
Ffam; PF00084; sushi; 2...
SMART; SM00032; CCP; 2...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31238 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane, Glycoprotein, SIGNAL 1 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%;
ilarity 50.0%;
Conservative 2
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243
262
275
78
185
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 261 CLIWORKWKKNR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWQREMRKVR 12
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275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
nes 6; Conser
                                                                                                                              SEQUENCE FROM N.A.
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DOMAIN
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DISULFID
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TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
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EMBL; AF147700; AAD33987.1; -.
EMBL; AE003712; AAF55285.1; -.
Flybase; FB00020629; nla.
SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;

8 2 2 2 3 S

Score 38; DB Pred. No. 14;

54.3%; 54.5%;

Query Match Best Local Similarity

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RCHINE-ZOIGNONE, PubMed=10731132,

RATAINE-BECKELED,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Gocay R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Gocay R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Adams M.D., Evans B.E., Richards S., Chen L.X.,

Randon R.C., Rogers Y.-H.C., Blazej K.G., Change M., Fefifer B.D.,

RA Ballaw R.M., Basu A., Baxendals J., Bayraktarold L., Beasley B.M.,

Rabeson K.Y., Bence P.V., Barana B.P., Handari D., Bolchhakov S.,

Rokova D., Botchan M.R., Boule J., Bayraktarold L., Beasley B.M.,

RA Burtis K.C., Bugam D.A., Paller H., Cadieu E., Center A., Chandra I.,

RA Cawley S., Delcher A., Deng Z., Mays A.D., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C.,

RA Doddek A., Goong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

RA Gordek A., Goong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

A Jahli M., Kalush F., Karpen G.H., Kez Z., Kennigon J.A., Ketchum K.A.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D.R., Moy M., Murphy B., Morberson D.,

Reiner S., Kolira C.D., Kraft C., Krait C., Krait C., Morris J., Moshrefi A.,

Rollson D.R., Nelson K.A., Liu J., Li Z., Liang Y., Inin X.,

Raland S., Ralanna G.S., Pan S., Pollard J., Puri V., Reese M.G.,

Reiner K., Remingron K., Sunder R.D.C., Scheeler F., Wang X.,

Mulliams S.M., Woodage T., Worley K., Wull Strong R., Sinth H.,

Rayer S., Spradling A.C., Staben C., Wull Strong R., Sinth H.,

Rayer S., Spradling A.C., Staben S., Cheeler F., Wang S., Zhan K., Shin R., Shin R., Shin R., Shin R., Shin R., Shin R., Shin R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Perygota; Neoptera; Endopterygota; Diptera; Brachyoera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                            #Cormick A.V., Goldberg M.L.;
"Gene required for elongation of Meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE. -!- SIMILARITY: BELONGS TO THE DSCR1 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                         MIA DROME STANDARD; PRT; 292 AA. 09XZL8; Q9V391; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                  Nebula protein.
                                                                                                                                                                                           NLA OR CG6072
                                                                                                                                                                                                                                                                                                                                                                              McCormick A.V
                                                                                                                                                                                                                                                                                                                                                                                                                                  females.
                           NLA_DROME
RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The Bub2-dependent mitotic pathway in yeast acts every cell cycle and
       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and prevents premature exit from mitosis. This cell-cycle arrest depends upon inhibition of the G-protein Teml by the BFAL/BUB2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulates cytokinesis.";
J. Cell Sci. 114:2345-2354(2001).
-!- FUNCTION: Part of a checkpoint which monitors spindle integrity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=91330299; PubMed=1651171;
Hoyt M.A., Totis L., Roberts B.T.;
S. cerevisiae genes required for cell cycle arrest in response to loss of microcubule function.";
Cell 66:507-517(1991).
                                                                                                                                                                                                                                                                                                                                                                     01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
11-AUG-1992 (Rel. 41, Last annotation update)
Mitotic check point protein BUB2 (Cell cycle arrest protein BUB2).
BUB2 OR YMR055C OR YM9796.08C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    [3]
MEDLINE=21385309; PubMed=11493673;
Lee S.E., Jensen S., Frenz L.M., Johnson A.L., Fesquet D., Johnston L.H.;
   3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=S288c / AB972;
Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00566; TBC; 1. SMART; SM00164; TBC; 1. Cell cycle; Mitosis. SEQUENCE 306 Aa; 35027 MW; Aldderseberrers CRC64;
                                                                                                                                                                                                                                                                                                           306 AA
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBUNIT: Interacts with BFA1.
-!- SUBCELLULAR LOCATION: Spindle poles.
-!- SIMILARITY: TO S.POMBE CDC16.
                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A39654; A39654.
SGD; S0004659; BUB2.
InterPro; IPR000195; RabGAP_TBC.
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   6; Conservative
                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                150 FOWLRSFRER 160
                                                                2 FOWOREMRKVR 12
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SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                           BUB2 YEAST
                                                                                                                                                                                                                                                                                                                                        P26448;
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Matches
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Gaps

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Indels

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Mismatches

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4; Conservative
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Matches
                                                                                                                                                                                                                       MAOX_RAT
                                                       8
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                                                                                                                                                                                                                                                                                                                                                           P48163; Q16855; Q9BWX8; Q9UIY4; Q9H1W3;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (Malic enzyme 1).
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 8-572 FROM N.A.
MEDLINE=96397682; PubMed=8804575;
Chou W.Y., Huang S.M., Chang G.G.;
"Nonidentity of the cDNA sequence of human breast cancer cell malic enzyme to that from the normal human cell.";
J. Protein Chem. 15:273-279 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Loeber G., Dworkin M.B., Infante A., Ahorn H.;
"Characterization of cytosolic malic enzyme in human tumor cells.";
FEBS Lett. 344:181-186(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2)
                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 572;
                       Length 306;
                                                                               3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   438 P -> S (IN REF. 2).
64149 MW; EA4C8CB36F6C619C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -:- SUBUNIT: HOMOTETRAMER.
-:- SUBCELLULAR LOCATION: Cytoplasmic.
-:- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NADP (BY SIMILARITY).
                       DB 1;
15;
                                                                                                                                                                                                                                                                                                                                       572 AA.
                       Score 38; DB
Pred. No. 15;
2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00072; MALOXRDTASE.
PROSITE; PS00331; MALIC_ENZYMES; 1.
                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=White adipose tissue;
MEDLINE=94244767; PubMed=8187880;
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Pfam; PF00390; malic; 1.
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                 54.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 27-572 FROM N.A.
                                                                               5; Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         318
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                                                                                                                                                                                            108 CFAWOTOORR 117
                       Query Match
Best Local Similarity
                                                                                                                                       1 CFQWQREMRK 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
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MAOX HUMAN

MAOX HUMAN

DT 01-FEB-
DT 01-FEB
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Best Local Similarity

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                                                                                                                                                                                                                                                                                                                            01-0AN-1990 (Rel. 13, Created)
01-APR-1993 (Rel. 25, Last sequence update)
15-7UN-2002 (Rel. 41, Last annotation update)
MADP-dependent malic enzyme (EC 1.1.1.40) (MADP-ME) (Malic enzyme 1).
MEI OR MOD1 OR MOD-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Morioka H., Magnuson M.A., Mitsuhashi T., Song M.K.H., Rall J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1-35 FROM N.A. MEDLINES-80906948; PubMed-3211151; MEDLINES-80906948; PubMed-3211151; MOTIOKA H., Tennyson G.E., Nikodem V.M.; "Structural and functional analysis of the rat malic enzyme gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nikodem V.M.;
"Structural characterization of the rat malic enzyme gene.";
Proc. Natl. Acad. Sci. U.S.A. 86:4912-4916(1989).
-!- CATALYTIC ACTIVITY: (S)-malate + NADP(+) = pyruvate + CO(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nikodem V.M., Magnuson M.A., Dozin B., Morioka H.; "Coding nucleotide sequence of rat malic enzyme mRNA and tissue specific regulation by thyroid hormone."; Endocr. Res. 15:547-564(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=Sprague-Dawley;
MEDINIDE=S611756; PubMed=3753699;
Magnuson M.A., Moricka H., Tecce M.F., Nikodem V.M.;
"Coding nucleotide sequence of rat liver malic enzyme mRNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SUBUNIT: HOMOTETRAMER.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE MALIC ENZYMES FAMILY.
                                                                                                                                                                                                                                                                         572 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE=90235791; PubMed=2699453;
                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mol. Cell. Biol. 8:3542-3545(1988)
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5.
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AAA41563.1;
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AAA41563.1;
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                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                          |: | |::|::
556 CYSWPEEVQKIQ 567
                                                          1 CFOWOREMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10116;
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M26590;
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"Methylmalonyl-CoA mutase from Propionibacterium shermanii. Evidence for the presence of two masked cysteine residues.";
Biochem. J. 260:339-343(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Propionibacterium freudenreichii shermanii.
Bacteria, Actinobacteria; Actinobacteria (class); Actinobacteridae;
Actinomycetales; Propionibacterineae; Propionibacteriaceae;
Propionibacterium.
NCBI_TAXID=1752;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mancia F., Keep N.H., Nakagawa A., Leadlay P.F., McSweeney S., Asmuusen B., Bosecke P., Diat O., Evans P.R.; McSweeney S. How coenzyme B12 radicals are generated: the crystal structure of methylmalonyl-coenzyme A mutase at 2-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NCIB 9885;
PubMed=9655823;
Mancia F., Evans P.R.;
Mancia F., Evans P.R.;
"Conformational changes on substrate binding to methylmalonyl CoA mutase and new insights into the free radical mechanism.";
Structure 6:711-720(1998).
-i. FUNCTION: CATALYZES THE ISOMENIZATION OF SUCCINYL-COA TO METHYLMALONYL-COA DURING SYNTHESIS OF PROPIONATE FROM TRICARBOXYLIC ACID-CYCLE INTERMEDIATES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marsh E.N., McKie N., Davis N.K., Leadlay P.F.; "Cloning and structural characterization of the genes coding for adenosylcobalamin-dependent methylmalonyl-CoA mutase from Propionibacterium shermanii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF 3-8; 95-99; 301-305; 472-477
                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-1989 (Rel. 12, Created)
01-0C7-1997 (Rel. 35, Last sequence update)
15-UTW-2002 (Rel. 41, Last annotation update)
Methylmalonyl-CoA mutase small subunit (RC 5.4.99.2) (MCB-beta)
                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                      54.3%; Score 38; DB 1; Length 572; 33.3%; Pred. No. 28; ive 5; Mismatches 3; Indels
                                                                                                                                                     NADP (BY SIMILARITY).
; 7D6EB48F3BA7D95B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 637 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
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                                                                              Pfam; PF00390; malic; 1.

PRINTS; PR00072; MALOXRDTASE.
PROSITE; PS00331; MALIC_ENZYMES; 1.
OXIGOTEGUCLASE; NADP.
NP_BIND 318 NADP (
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STRAIN-NCIB 9885;
MEDLINE-89350815; PubMed=2569860;
EMBL; M26591; AAA41563.1; JOINED.
BRBL; M26592; AAA41563.1; JOINED.
EMBL; M26593; AAA41563.1; JOINED.
PIR; A37228; DERTMX.
                                                                interPro; IPR001891; Malic_oxred.
                                                                                                                                                     NP_BIND 301 318 NA
SEQUENCE 572 AA; 64002 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biochem. J. 260:345-352(1989).
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Best Local Similarity
Matches 4; Conserv
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P11652;
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Rhabditidae; Peloderinae; Caenorhabditis.
CATALYTIC ACTIVITY: (R)-2-methyl-3-oxopropancyl-CoA = succinyl-
                                                  -i- PATHWAY: Propionic acid fermentation.
-i- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-i- SIMILARITY: BELONGS TO THE METHYLMALONYL-COA MUTASE FAMILY.
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-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54.3%; Score 38; DB 1; Length 637; 66.7%; Pred. No. 31; ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Durbin R.; Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
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15-DEC-1998 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Hypothetical protein R13G10.2 in chromosome III.
R13G10.2.
                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001629; MM COA mutase.
InterPro; IPR004608; MmCOA mut beta.
Pfam; PF01642; MM COA mutase; I.
TIGRFAMS; TIGR00642; mmCOA mut beta; 1.
PROSITE; PS00544; METMALONYL COA MUTASE; I.
ISOMERASE; Vitamin B12; CObalt; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                     -!- COFACTOR: ADENOSYLCOBALAMIN.
                                                                                                                                                                                                                                                                     EMBL; X14965; CAA33089.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                     1REQ; 27-JAN-97.
2REQ; 24-JAN-98.
3REQ; 24-JUN-98.
4REQ; 13-JAN-99.
6REQ; 09-SEP-98.
7REQ; 16-SEP-98.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 QWQREMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33 QWEREVEKV 41
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PIR; S18910; S18910.
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SEQUENCE
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Lye R.J., Wilson R.K., Waterston R.H.;
"Genomic structure of a cytoplasmic dynein heavy chain gene from the nematode Caenorhabditis elegans.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
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                                                                                                                                                                                             54.3%; Score 38; DB 1; Length 783; 50.0%; Pred. No. 38; tive 2; Mismatches 4; Indels
                                      EMBL; Z35602; CAA84671.2; -...
Wormbey, R13G10.2; CES5088.
InterPro; IRS002937, Amino oxidase.
Pfam; PF01593; Amino oxidase; 1.
Hypothetical protein; Oxidoreductase; Flavoprotein; FAD. NP BLND
PRIND
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SEQUENCE 783 AA; 88799 MW; 8D087E96464DC908 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Du Z., Maggi L.;
Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Last sequence update) 15-JUM-2002 (Rel. 41, Last annotation update) Dynein heavy chain, cytosolic (DYHC). DHC-1 OR T21E12.4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cell Motil. Cytoskeleton 32:26-36(1995).
      or send an email to license@isb-sib.ch).
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InterPro; IPR004593; AAA ATPase.
InterPro; IPR004273; Dynein_heavy.
Pfam; PP03028; Dynein heavy; 1.
SWART; SM00382; AAA; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
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                                                                                                                                                                                                                   Local Similarity 50.0
les 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                 540 CIDWGRDDRKVK 551
                                                                                                                                                                                                                                                                            1 CFOWOREMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
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Q19020;
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-1- FUNCTION: RECEPTOR FOR INTERLEUKIN-2.
-1- SUBGNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
-1- SUBGNIT: NON COVALENT DIMER OF A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
WITH A GAMMA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=22241682; PubMed=1572550;
Bujdoos R., Sargan D.R., Williamson M.L., McConnell I.;
Bujdoos R., Sargan D.R., Williamson M.L., McConnell I.;
Eloning of a cDNA encoding the ovine interleukin-2 receptor 55-kDa protein, CD25.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoldea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-PRB-1996 (Rel. 33, Last annotation update)
Interleukin-2 receptor alpha chain precursor (IL-2 receptor alpha subunit) (P55) (TAC antigen) (CD25).
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MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
COLLED COLL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                      Length 4568;
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54.5%; Pred. No. 2.3e+02;
ive 3; Mismatches 2; Indels
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                         (POTENTIAL).
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-!- SIMILARITY: CONTAINS 2 SUSHI (SCR) DOMAINS.
                                                                                                                                                                                                                                                              (POTENTIAL).
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Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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245 CNRWVKEIRKV 255
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hes 6; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI TaxID=9940;
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Search completed: February 21, 2003, 07:28:01 Job time : 5.6 secs

1 CFQWQREMRKVR 12 | | | | | | 272 261 CLTWQRRWKKNR 272

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Gaps

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Query Match 52.9%; Score 37; DB 1; Length 275; Best Local Similarity 50.0%; Pred. No. 20; Matches 6; Conservative 1; Mismatches 5; Indels

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Q19153 caenorhabdi
Q91v34 neisseria m
Q9xfd5 oryza sativ
Q9sml2 cicer ariet
Q95f7y4 salmonella
Q08580 saccharomyc
Q98680 saccharomyc
Q9662 agrobacteri
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 097tq8 clostridium 09hpa3 halobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBtcd2 homo sapien
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                                                                         (without alignments)
118.873 Million cell updates/sec
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                                                              February 21, 2003, 07:25:55 ; Search time 20.8 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9ucy5 ]
Q9tr80 (
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                 671580 segs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
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Q9HPA3
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Q9SML2
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Q8U6F2
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Q9XFD5
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Q9UCY5
Q9TR80
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                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                         sp_rodent:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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Q08580
                                                                                                                                                                                                                                                                                                                                              sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 2000000000
                                                                                                        US-09-743-107B-86
                                                                                                                            1 CFQWQREMRKVR 12
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Match Length DB
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No.
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5 Q9NE65 16 Q8U5K3 4 Q8WYX2 16 Q8KSE2 16 Q9CHM1	4 Q8TAX2 Q8tax2 homo sapie 12 Q9QB73 Q9qb73 yaba monk 10 Q24366 Q94366 Spiazwa 4 Q9NZW0 Q9nZW0 Appies 4 Q9NZW3 Q9nZW3 Appies 4 Q9NZW2 Q9nus2 Q9nus2	2 Q9ERU5 16 P96223 6 Q95R28 10 Q22185 10 Q2LTD4 10 Q22188 4 O94937 2 Q953R7	0.5575 0.5563 0.86216 0.52003 0.95743 0.77855 0.77855 0.8555
55.45.7 5.45.3 5.45.3 5.65.5 6.55.5 7	24 24 24 24 24 24 24 24 24 24 24 24 24 2		
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ALIGNMENTS

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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0
                                                                                                                                                                                                                                                                         Length 711;
                                                                                                                                                               SEQUENCE FROM N.A.
TISSUB-PROSTATE;
StraubBorg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC022347; AAH22347.1; --
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                       1; Indels
                         01-UNN-2002 (TrEMBLrel. 21, Created)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-UUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UJN-2001 (TrEMBLrel. 17, Last annotation update)
Lactroferrin homolog (Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                                                       85.7%; Score 60; DB 4;
90.9%; Pred. No. 0.022;
iive 0; Mismatches
 711 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                             38 A.A.
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                       Best Local Similarity 90.9
Matches 10; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                     1 CFOWOREMRKV 11
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                                                                          Lactotransferrin.
                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                         Query Match
Q8TCD2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9UCY5
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"Molecular cloning of 11S globulin and 2S albumin, the two major seed
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Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
Clostridiales; Clostridiaceae; Clostridium.
NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                             57.1%; Score 40; DB 10; Length 148; 66.7%; Pred. No. 15; 3; Indels ive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57.1%; Score 40; DB 5; Length 275; 63.6%; Pred. No. 29; ive 1; Mismatches 3; Indels
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01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-OTUN-2002 (TrEMBLrel. 21, Last annotation update)
Xre family DNA-binding domain and TPR repeats containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DODEON K.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                            Pfam; PF00234; tryp_alpha_amyl̄; 1.
PRINYS; PR00496; NAPIN.
SMART; SM00499; AAI; 1.
SEQUENCE 148 AA; 17524 MW; BA46B033BA13E3DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           investigating biology.";
Science 282:2012-2018 [1998).
BMBL; Z81089; CAB01137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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                                  storage proteins in sesame.";
J. Agric. Food Chem. 47:4932-4938(1999)
EMBL; AF091841; AAD42943.1; -.
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01-AUG-1998 (TrEMBLrel. 07, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last anno
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MEDLINE=99069613; PubMed=9851916;
                                                                                                                       InterPro; IPR003612; AAI.
InterPro; IPR000617; Napin.
InterPro; IPR001768; Try/amyl_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clostridium acetobutylicum.
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Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Lag 6, Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWQREMR 9
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ID 09
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterida I; Lamiales; Pedaliaceae; Sesamum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Caprinae, Ovis.
                                                                                                                                                                             "Characterization of the 84-kDa protein with ABH activity in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
0
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 56; DB 4; Length 38;
Pred. No. 0.0059;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                              InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 1.
SEQUENCE 38 AA, 4459 MW; 0402F490B5EBDDEB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=95127729; PubMed=7827104;
Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP; O77698; 1CB2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen E.C.F., Tzen J.T.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74.3%; Score 52; DB 6; 63.6%; Pred. No. 0.026; iive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33 AA.
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                                                                                                                                                                                                         seminal plasma.";
Jpn. J. Legal Med. 49:281-293(1995)
HSSP; P02788; 1BKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                    MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001156; Transferrin.
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Best Local Similarity
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                                                                                     SEQUENCE FROM N.A.
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                               NCBI_TaxID=9606;
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01-JUN-2001
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Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBL_TaxID=65699;
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STRAIN=22491 / SEROGROUP A / SEROTYPE 4A;

MEDLINB=20202556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,

Jagels K., Leather S., Moule S., Mingall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,

Whitchead S., Spratt B.G., Barrell B.G.;

"Complete DNA sequence of a serogroup A strain of Neisseria
                                                                                                                                       Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57.1%; Score 40; DB 5; Length 932; 63.6%; Pred. No. 99; ative 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R.;
"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Direct Submission.";
"Maga4025.1; -..
"InterPro; IPR000731; HMGCR/patch_5TM.
PROSITE; PS50156; SSD; 1.
Hypothetical protein.
SEQUENCE 932 AA; 105144 MW; 66680619ADACBFD5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=BRISTOL N2;
Favello A., Gattung S.,
"The sequence of C. elegans cosmid F07C3.";
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein, Complete proteome.
SEQUENCE 57 AA; 6491 MW; A6DB781C29E212C5 CRC64;
      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 105.1 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Hypothetical protein NMA1014.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57 AA.
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MEDLINE-99069613; PubMed-9851916;
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Nature 404:502-506(2000).
EMBL; AL162754; CAB84283.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                Caenorhabditis elegans.
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                                                                                                                                                                                                                             SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                  NCBI TaxID=6239;
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               STRAIN=ATCC 824 / DSM 792 / VKM B-1787;

X MEDLINE=21359325; PubMed=11466286;

A Gibson R., is the H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

A Gibson R., is abathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

A Bennett G.N., Koonin E.V., Smith D.R.;

B Hannett G.N., Koonin E.V., Smith D.R.;

B Genome sequence and comparative analysis of the solvent-producing to Bacterium Glostridium acetobutylicum.";

J. Bacterium Glostridium acetobutylicum.";

J. Bacteriol. 183:4823-4838(2001).

R EMBL; AEO01438; ARX76786.1;

R InterPro; IPR001440; TPR.

R SMART; SM00230; HTH XRE; 1.

R SMART; SM0028; TPR. 3.

DA-binding; Plasmid; Complete protecome.
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MEDLINE-20504483; PubMed=11016950;
NG W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
Swartzell S., Weir D., Hall J., Dall T.A., Welti R., Goo Y.A.,
Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
"Genome sequence of Halobacterium species NRC-1.",
"Genome Scquence of Halobacterium species NRC-1.",
"BMEL, ARCOSONS, AAC199671; -
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                          57.1%; Score 40; DB 16; Length 443; 50.0%; Pred. No. 47; 2; Indels ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57.1%; Score 40; DB 17; Length 584; 41.7%; Pred. No. 62;
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Halobacteriaceae, Halobacterium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584 AA.
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InterPro; IPR001622; K+channel_pore.
Pfam; PF00805; Pentapeptide; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Halobacterium sp. (strain NRC-1).
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Best Local Similarity 50.0°
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 41.7
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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SEQUENCE FROM N.A.
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Q9HPA3

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RESULT 8 Q19153 ID Q1 AC Q1

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Cicer arietinum (Chickpea) (Garbanzo).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids I; Fabales, Fabaceae, Papilionoideae, Cicereae, Cicer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Overkamp S., Hein F., Barz W.;

Cloning and characterization of eight cytochrome P450 cDNAs from cloidypea (Gicer ariethnum L.) cell suspension cultures.";

Plant Sci. 155:101-108 (2000).

-! SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.

EMBL; AJ248800; CAB56742.1;

InterPro; IPR001128; Cytochrome_P450.

Pfam; PR0067; p450;

PRINTS; PR00385; P450.
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Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                        Score 39; DB 10; Length 207;
Fred. No. 33;
2; Mismatches 0; Indels
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Pfam; PF00067; p450; 1.

PRINTS; PR00385; P450.

PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.

Heme; Monocxygename; Oxidoreductase.

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SEQÜENCE 207 AA; 23476 MW; DEID9AAAEC2D1BFB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       240 AA; 27150 MW; 19CB488E6E7C0407 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN=CV. ILC 3279; TISSUE=CELL SUSPENSION CULTURE;
PubMed=10773344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
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Heme; Monooxygenase; Oxidoreductase.
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01-MAR-2001 (TrEMBLrel. 16, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-MAR-2002 (TrEMBLrel. 20, Last ann
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                                                                                                                                                                                                               Query Match 55.7%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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eurosids I; Fabales; Fabaceae; Papilionoideae; Cicereae; Cicer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Liu J., Yang J.;
"Suppression subtractive hybridization (SSH) identified candidate subpression subtractive hybridization (SSH) identified candidate sense that are differentially expressed at rice young panicle.";
Submitted (ARE-1999) to the EMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
Interpro. PRO01128; Cytochrome_P450.
Pfam; PF00067; p450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME P450; UNKNOWN_1.
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Overkants), Hein F., Barz W.;
Cloning and characterization of eight cytochrome P450 cDNas from chickpea (cicer arietinum L.) cell suspension cultures.";
Plant Sci. 155:101-108 (2000).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
BMBL, AJ249801; CAB56743.1;
-InterPro; IPR001128; Cytochrome_P450.
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         DB 16; Length 57;
                                                                  3; Indels
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STRAIN=CV. ILC 3279; TISSUE=CELL SUSPENSION CULTURE;
PubMed=10773344;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NAR-2002 (TrEMBLrel. 20, Last annotation update)
Cytochrome P450 (Fragment).
                                                                                                                                                                                                                                                                                                                                              105 AA.
   Query Match
Best Local Similarity 66.7%; Pred. No. 8.9;
Matches 8; Conservative 1; Mismatches
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Search completed: February 21, 2003, 07:44:40 Job time : 21.8 secs
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                                                                                                                                                                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
Rychlik I., Sebkova A.; "Plasmid pJ of Salmonella enteritidis encoding hypothetical rep
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                        protein.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF268389; AAG17348.1; -.
InterPro; IPR000989; Rep.
Pfam; PF01446; Rep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Hughes B., Pohl T.M.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
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SGD; S0005719; YOR193W.
SEQUENCE 376 AA; 44131 MW; 976FDBCA43AB4F80 CRC64;
                                                                                                     329 AA; 37819 MW; C3D88A9C0175155D CRC64;
                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ORF YOR193W.
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181 FRWLREMKKL 190
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Q08580;
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Sequence features of the regions of 1,011,550 bp covered by seventeen P1 and TAC clones.";
DNA Res. 6:183-195(1999).
EMBI, ABBO9113; BABBO9175.1; -.
SEQUENCE 866 AA; 100187 MW; 164FAB9B4976D27D CRC64;
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                                                                                                                                  February 21, 2003, 07:37:21 ; Search time 28.093 Seconds (without alignments) 56.918 Million cell updates/sec
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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ALIGNMENTS

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Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                                              Dolphin GT;
                                                                Human lactoferrin derived peptide SEQ ID NO:72.
                                                                                                                                                                                                                                                                                                              Hanson LA, Mattsby-Baltzer I, Baltzer L,
AAY78072 standard; Peptide; 12 AA.
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98SE-0002562.
98SE-0004614.
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                                          (first entry)
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                                                                                                                                                                           WO200001730-A1
                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                    17-JUL-1998;
29-DEC-1998;
                                                                                                                                                                                                                      06-JUL-1999;
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                                          25-APR-2000
                                                                                                                                                                                                13-JAN-2000.
                                                                                                                                                        Synthetic.
                    AAY78072;
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AAY78001 to AAY78100 represent peptides having sequences based on human
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                                                                                                                                                                                                                                                                                                                             WPI; 2000-147388/13.
                                                                                                          12 AA;
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                                                                                                                                                                                                                                  lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported binding to specific lactoferrin receptors and are then transported through the direction. A medicinal product of the peptide or fragment can be used for treating and colitis, and Candida infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                         AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human, lactoferrin, modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.5%; Score 66; DB 21; Length 12; 91.7%; Pred. No. 3.1e-05; ive 0; Mismatches 1; Indels
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                                                                                                                            Claim 22; Page 35; 102pp; English.
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        binding to specific lattoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and way also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used callincally on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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lactoferrin. The peptides are taken up in the intestine through
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91.7%; Pred. No. 4.7e-05;
ive 0; Mismatches 1; Indels
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98SE-0002562.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/of prevention of infections (such as urinary tract infections, colltis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
                                Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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   may also be used as preservatives.
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                                                                                                                                                                                                                                                                                                                                                 Score 65; DB 21;
Pred. No. 4.7e-05;
0; Mismatches 1;
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fungicidal and bactericidal and
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98SE-0004614.
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29-DEC-1998;
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through lactoferrin. The peptides are taken up in the intestine through the opecific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, onlitis, and candida infections a memorsal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower canble them to be used for the same purposes as lactoferrin at lower
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                                             Score 65; DB 21; Length 12;
Pred. No. 4.7e-05;
0; Mismatches 1; Indels
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                                                                                 0; Mismatches
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                                             97.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                         bactericidal; preservative.
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Best Local Similarity 91.74
                                                              Local Similarity 91.7
nes 11; Conservative
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                12 AA;
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AAY78088 standard; Peptide; 12

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AAY78088;

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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported binding to specific lactoferrin receptors and are then transported through the direculation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would anable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                   AAY78087 standard; Peptide; 12 AA.
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98SE-0002562.
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                              1 CFOWERNMRKVR 12
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CFQWXRNMRKVR
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the circulation. A medicinal product of the peptide or fragment through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also any though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                          Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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100.0%; Pred. No. 4.7e-05;
ive 0; Mismatches 0; Indels
                                                                                              Human lactoferrin derived peptide SEQ ID NO:88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baltzer L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hanson LA, Mattsby-Baltzer I,
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98SE-0002562.
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nes 12; Conservative
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                                                                                                                                                                                                                    Homo sapiens.
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29-DEC-1998;
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                                                                                                                                                                                                                                       Synthetic.
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Human lactoferrin derived peptide SEQ ID NO:91.

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Gaps 0;

12; Conservative

Matches

Best Local Similarity

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RESULT 7

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us-09-743-107b-87.rag

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Human, lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                                                                                                                                                                                                                                          97.0%; Score 65; DB 21; Length 12; 91.7%; Pred. No. 4.7e-05; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human lactoferrin derived peptide SEQ ID NO:92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY78092 standard; Peptide; 12 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                              (ASCI-) A+ SCI INVEST AB.
                                                                                                                                                                                                                                                                                                                                                                                          11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         1 CFQWXRNMRKVR 12
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            12 AA;
                                                                  WO200001730-A1.
                                            Homo sapiens
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                                                                                                06-JUL-1999;
                                                                                                               06-JUL-1998;
                                                                                                                        17-JUL-1998;
29-DEC-1998;
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                                                                                 13-JAN-2000
                                                    Synthetic.
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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98SE-0004614.
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 22; Page 38; 102pp; English

Baltzer L,

Hanson LA, Mattsby-Baltzer I,

WPI; 2000-147388/13.

(ASCI-) A+ SCI INVEST AB

98SE-0002441. 98SE-0004614.

99WO-SE01230

06-JUL-1999; 06-JUL-1998; 29-DEC-1998;

13-JAN-2000

WO200001730-A1

Synthetic.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through the intential clactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower ceals.
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
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Pred. No. 4.7e-05;
); Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
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Best Local Similarity
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Gaps 0 Θ

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Mattsby-Baltzer I,
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Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                        1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                             2 CFOWORNMRKVR 13
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                    WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                         13 AA;
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Hanson LA,
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                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                    cost.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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                                                                                                                  New peptides used for treatment and prevention of infections inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                      Score 65; DB 21; Length 13;
Pred. No. 5e-05;
0; Mismatches 1; Indels
                                                                         Baltzer L, Dolphin GT;
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                                                                                                                                                Claim 12; Page 70; 102pp; English
                                                                        Hanson LA, Mattsby-Baltzer I,
                                                                                                                                                                                                                                                                                                                                                                      97.0%;
91.7%;
                   98SE-0002562.
98SE-0004614.
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        98SE-0002441.
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98SE-0004614.
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                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                  (ASCI-) A+ SCI INVEST AB.
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                                                                                            WPI; 2000-147388/13.
                                                                                                                                                                                                                                                                                                                                                  13 AA;
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         06-JUL-1998;
                             29-DEC-1998;
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29-DEC-1998;
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lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                     AAY78001 to AAY78100 represent peptides having sequences based on human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                                                                                                                                            New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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Pred. No. 5e-05;
0; Mismatches 1; Indels
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Dolphin GT;
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Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baltzer L,
                                                                                                                                                                                                                                                                Claim 15; Page 74; 102pp; English.
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98SE-0002562.
98SE-0004614.
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                    AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired
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                                                                                                                                                anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservativa
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                                                                                                                                                                                                                                                  Score 65; DB 21; Length 13;
Pred. No. 5e-05;
                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dolphin GT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human lactoferrin derived peptide SEQ ID NO:36.
                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                    AAY78036 standard; Peptide; 14 AA.
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 Claim 18; Page 74; 102pp; English.
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91.7%;
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98SE-0004614.
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Best Local Similarity 91.7
Matches 11, Conservative
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29-DEC-1998;
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Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infections and anti-tumoural properties they cannot be used clinically on a broad basis because of high production
urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                         97.0%; Score 65; DB 21; Length 14; 91.7%; Pred. No. 5.4e-05; ive 0; Mismatches 1; Indels
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98SE-0002562.
98SE-0004614.
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costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                     cost.
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14 AA; Sequence

Gaps ; 0 Score 65; DB 21; Length 14; Pred. No. 5.4e-05; 0; Mismatches 1; Indels 97.0%; Query Match 97.0 Best Local Similarity 91.7 Matches 11; Conservative

1 CFQWXRNMRKVR 12 ð

3 CFÓWORNMRKVR 14

RESULT 15 AAY78051

AAY78051 standard; Peptide; 14 AA.

AAY78051;

25-APR-2000 (first entry)

Human lactoferrin derived peptide SEQ ID NO:51.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colltis; Candida infection; fungicidal; bactericidal; preservative

Homo sapiens.

Synthetic.

WO200001730-A1.

13-JAN-2000

99WO-SE01230. 06-JUL-1999;

98SE-0002441. 98SE-0002562. 98SE-0004614. 06-JUL-1998; 17-JUL-1998; 29-DEC-1998;

(ASCI-) A+ SCI INVEST AB.

Dolphin GT; Baltzer L, Mattsby-Baltzer I, Hanson LA,

WPI; 2000-147388/13.

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 18; Page 75; 102pp; English.

AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also thugicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and continued them.

14 AA; Sequence

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1 CFQWXRNMRKVR 12 ð

3 CFOWORNMRKVR 14

Search completed: February 21, 2003, 07:56:42 Job time : 28.093 secs

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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FUN-019
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTER.FILCS:
LENGTH: 18 amino acids
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
TYPE: amino acid
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                                                              February 21, 2003, 07:50:40 ; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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Sequence 3,
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-475-055-8
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Maximum Match 100%
Listing first 45 summaries
                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match Length DB
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NAME/KEY: Peptide LOCATION: 1..18 OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE

TOPOLOGY: linear MOLECULE TYPE: peptide

OLIFERATION URWITZ &	Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli	म् म् म् म् म् म् त्रात्रात्रात्रात	
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US-08-628-380-8
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                                                                                                                                                                                                                                                           Sequence 8, Application US/08485948

Patent No. 5855802

GENERAL INFORMATION:

APPLICANT: YOUG MING LI

APPLICANT: HELEN VLASSARA

APPLICANT: ANTHONY CERAM!

TITLE OF INVENTION: ENDPRODUCTS; AND METHODS OF THEIR USE
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                                                 Score 65; DB 1; Length 18; Pred. No. 3.6e-05; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26,742
FR: 947-1-008A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
CLASSIFICATION: 436
PRIOR APPLICATION UNMER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 25,742
REFERENCE/DOCKET NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-0
TELECPHONE: 201 489-5800
TELECPHONE: 201 489-5800
TELECPHONE: 201 489-5800
TELECPHONE: 201 343-1684
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
FUNCTH: 18 mmino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
(20-37)"
                                                     97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DIAMETER TYPE: Deptide
Communication: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best_Local Similarity 91.7
Matches 11, Conservative
                                                 Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWXRNMRKVR 12
OTHER INFORMATION:
                                                                                                                             1 CFOWXRNMRKVR 12
                                                                                                                                                                     1 CFOWORNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-485-948-8
                                                                                                                                                                                                                             RESULT 2
US-08-485-948-8
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US-08-204-487-3
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1 CFOWORNMRKVR 12

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Use decreased by Application US/0862380

Sequence A Application US/0862380

Patent No. 8632131

Patent No. 86321313

Patent No. 863213131

Patent No.
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: modified site
LOCATION:
2
LIDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.0%; Score 65; DB 1; Length 20;
                                                                            19910905
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PILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755
CLASSIPICATION 530
FILING DATE: 19910905
CLASSIPICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek JT.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 19
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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IMMEDIATE SOURCE:
LIBRARY:
CLONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-755-161A-3
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                                                                                                                                                                                                                                                                                                                                                  OFFWARE PATENTING STSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILING DATE:
FILING DATE:
CLASSITCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,948
FILING DATE:
APPLICATION NUMBER: 08/485,17
FILING DATE:
APPLICATION NUMBER: 08/489,217
FILING DATE:
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
RELEPHONE: 201 487-5800
TELLEPAK: 201 343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 65; DB 2; I
Pred. No. 3.6e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Wenderoth, Lind & Ponack STREET: 805 Fifteenth Street, N.W., #700 CITY: Washington STATE: D.C. COUNTRY: U.S.A. ZIP: 20005 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDLION TYPE: PLOSDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/07755161A Patent No. 5304633
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: actrical TELEFAX: actrical TELEX: 133521
INFORMATION FOR SEQ ID NO: B: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acids TYPE: amino acids STRANDEDNESS: single modulogy: linear length acids actrical modulogy: linear length acids actrical modulogy: linear length acids actrical actrical linear length actrical linear le
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Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLRCULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11; Conservative
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US-07-755-161A-3
                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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us-09-743-107b-87.rai

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NAME/KEY: modified site
LOCATION: 19
LOCATION: 19
LOCATION: 19
CTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: (ys residue at location 19 connected by disulfide bond with
OTHER INFORMATION:
OTHER INFORMATION:
                                   OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
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Pred. No. 4e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: MOSUCHI, WATARU
APPLICANT: TANAKA, SHIGEAKI
APPLICANT: KAMASKI, YOSHIMIRO
APPLICANT: KAMASKI, YOSHIMIRO
APPLICANT: WITHON: UCHIDA, TOSHIMIRO
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT STREET: 53 STATE STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 02-MAR-1994
CLASSIFICATION: 514
ATTORNEY/AGENI INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,503
REFERENCE/DOCKET NUMBER: FJN-019
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/204,487 FILING DATE: 02-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PUBLICATION DATE: RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08204487
Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: YAMAMOTO, NAOKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 CFOWORINMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE
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                                                                                                                                                                                                                                                                                                                                           JOURNAL:
                                                                                                                                                                                                                                                                                                AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-07-891-174-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 7
US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                               VOLUME:
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Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                         APPLICANT: Mamoru TOWITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an
TITLE OF INVENTION: Antimicrobial Agent
                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: D.C.
COUTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                             ; Sequence 3, Application US/07891174; Patent No. 5317084 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT; Mamoru TOMITA et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Warren M. Cheek Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                 Best Local Similarity 91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: 202-371-885
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE:
                                                                                                               2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                                              1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INDIVIDUAL ISOLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LIBRARY:
                                                                                                                                                                                                           US-07-891-174-3
                                        Matches
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us-09-743-107b-87.rai

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US-08-256-771-24
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US-08-381-984-24
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Patent No. 5656591
GENERAL INPORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                                                                                                          Query Match
97.0%; Score 65; DB 1; Length 20;
Best Local Similarity 91.7%; Pred. No. 4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "Cys residues are linked by OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                            ; LOCATION: 1..20; OTHER INFORMATION: /note= "ANTIBACTERIAL PEPTIDE; OTHER INFORMATION: DERIVED FROM HUMAN LACTOFERRIN" US-08-204-487-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/256,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WALTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/25
FILING DATE: July 22, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION WUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 24: SEQUENCE CHARACTERISTICS:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 amino acids
                                                                                                        single
                                                                                                                                             MOLECULE TYPE: peptide
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                                                                                                                                                                                      NAME/KEY: Peptide
                                                                                                                                                                                                                                                                                                                                                                                               1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CFÓWORNMRKVR 13
                                                                                TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid STRANDEDNESS: sin
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                                                                                                                            TOPOLOGY:
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US-08-256-771-24
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US-08-256-771-25
IS-Quence 25. Application US/08256771
| Sequence 25. Application US/08256771
| GENERAL INFORMATION:
| APPLICANT: Mamoru TOMITA et al. |
| TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING |
| TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING |
| TITLE OF INVENTION: PRODUCTS THEREWITH |
| NUMBER OF SEQUENCES: 32 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Wenderoth, Lind & Ponack |
| STREET: 805 Fifteenth Street, N.W., #700 |
| CITY: Washington
                                                     0
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US-08-256-771-25
    Score 65, DB 1; Length 20;
Pred. No. 4e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 97.0%; Score 65; DB 1; Length 20; Best Local Similarity 91.7%; Pred. No. 4e-05; Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: JULY 22, 1994
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WATTEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
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. Cheek, or
33,367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 amino acids
                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss: single
linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
IDENTIFICATION METHOD:
                                                                                             1 CFQWXRNMRKVR 12
                                                                                                                                     2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CPOWXRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: si
Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RY: U.S.A.
20005
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APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
TITLE OF INVENTION: useful microorganism thereof
FILE REPERSIVE: PA/SY6/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 1990-05-14
PRIOR APPLICATION NUMBER: PCT/KR99/00373
PRIOR FILING DATE: 1998-07-14
PRIOR APPLICATION NUMBER: KR1998-29351
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "the specified peptide as well as peptides including the specified peptide as a fragment there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IDENTIFICATION METHOD:
OCHER INFORMATION: /note= "cysteine residues at positions 2
(OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
US-08-381-984-25
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                                                                                                        COMPUTER ERADABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: TBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Mordperfect 5.1
CURRENT APPLICATION DATA:
  805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/381,984
FILING DATE: APTI 11, 1995
FILING SEPECATION: 252
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-508-734-4
'Sequence 4, Application US/09508734
'Patent No. 6423509
                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
RECISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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OTHER INFORMATION: /n
OTHER INFORMATION: pe
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                                                             RY: U.S.A.
20005
                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: si
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OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment thered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 1; Length 20;
Pred. No. 4e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA: APPLICATION NOWER: US/08/381,984 FILLING DATE: APPTI 11, 1995 CLASSIFICATION: 252
                                                                                                                                                          ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25, Application US/08381984
Patent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE 32
ADDRESSEE: Wenderoth, Lind & Ponack
Sequence 24, Application US/08381984
                     Patent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cheek, Jr.
3ER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
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91.7%;
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NAME: Warren M. Cheek, J.
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 91.7
Matches 11; Conservative
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWXRNMRKVR 12
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                                                                                                                                                                                                                                                   U.S.A.
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                                                                                                                                                                                                                             STATE: D.C
                                                                                                                                                                                                                                                                      20005
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US-08-381-984-25
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                                                                                                                                                                                                                                                   COUNTRY:
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NAME/KEY: modified site
LOCATION: 21
IDENTIFICATION METHOD:
OTHER INFORMATION: (by residue at location 21 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 4"
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LOCATION: 4
LIDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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PUBLICATION DATE:

RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                      33,367
                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION
TELEPHONE: 202-371-8850
                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 10:
  FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Jr
REGISTRATION NUMBER: 33,
                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLLOGY: linear
MOLECULE TYPE:
                                                                                                                                 TELEFAX: 202-371-885
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: the PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE:
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CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INDIVIDUAL ISOLATE
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IMMEDIATE SOURCE:
LIBRARY:
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                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE TYPE:
CELL TYPE:
CELL LINE:
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UNITS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VOLUME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN:
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APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANT: Samyang Genex Corporation
APPLICANTON: Wass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REFERENCE: PA/SYG/00139
CURRENT APPLICANTON WUMBER: US/09/508,734
CURRENT FILING DATE: 1099-07-14
PRIOR APPLICATION NUMBER: ECT/KR99/00373
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR APPLICATION NUMBER: KR1998-29351
PRIOR APPLICATION NUMBER: KR1998-29351
SOFTWARE: KOPATENT 1.71
SEQ ID NO 6
IENGTH: 24
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                                                                                                     Query Match 97.0%; Score 65; DB 4; Length 22; Best Local Similarity 91.7%; Pred. No. 4.4e-05; Matches 11; Conservative 0; Mismatches 1; Indels
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Sequence 10, Application US/07755161A

Patent No. 5346433

GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb COMPUTER: TBM COMPATIBLE OPERATING SYSTEM: MS-DOS SOFTWARE: DisplayWrite CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/07/755,161A
                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/09508734 Patent No. 6423509
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                  ; TYPE: PRT
; ORGANISM: Homo Bapiens
US-09-508-734-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-09-508-734-6
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STATE: D.C.
COUNTRY: U.S.A.
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Best Local Similarity
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LENGTH: 22
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POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY: modified site
LOCATION:
LOCATION:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
               Sequence 10, Application US/07891174

Patent No. 5317084

GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITILE OF INVENTION: Antimicrobial Peptides and an ITILE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                          STATE: "GENERAL STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER REALABLE FORM:
MEDIUM TYPE: Diskette, S.25 inch, 500Kb
COMPUTER: IBM Compartable
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION DATA:
APPLICATION NUMBER: US,07/755,161
FILING DATE: 05-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek Ur.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION NUMBER:
TELECOMMUNICATION NUMBER:
TELECOMMUNICATION NUMBER:
TELEFRANCE/DOCKET NUMBER:
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21
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SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
TYPE: amino acid
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TOPOLOGY: linear
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DEVELOPMENTAL STAGE:
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CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
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ORIGINAL SOURCE:
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HYPOTHETICAL:
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NAME/KEY:
LOCATION:
US-07-891-174-10
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" AUTHORS AUTHORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 21, 2003, 08:04:25 Job time: 8.93023 secs
                                                                                                                                                                                                                                                                             FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWXRNMRKVR 12
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                                                                                                                                                                                                                                                           DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                               US-07-891-174-10
                                                                                                                            TITLE:
JOURNAL:
                                                                                                                                                                       VOLUME:
                                                                                                                                                                                                                    PAGES:
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us-09-743-107b-87.rapb

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(without alignments)
54.162 Million cell updates/sec
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(ggn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
(ggn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
(ggn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
(ggn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
(ggn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              156504 seqs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Published Applications AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                   OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                   Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	65	97.0	15	! 6	TS-09-798-869-2	iland Capacimes
10	7	97.0	25	, σ	118-09-798-869-20	. 0
lm	65	97.0	694	n on	US-10-023-096-2	
4	57	85.1	15	0	0-698-862-60-SN	įψ
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9	48	71.6	25	9	US-09-798-869-23	23
7	40	59.7	15	σ	US-09-798-869-7	•
80	33	58.2	15	σ	US-09-798-869-4	4
6	39	58.2	25	σ	US-09-798-869-22	22.
10	37	55.2	489	σ	US-09-888-320-2	2, A
11	36	53.7	15	σ	8-698-862-60-SD	ω,
12	36	53.7	15	σ	US-09-798-869-29	29
13	36	53.7	15	σ	US-09-798-869-30	30,
14	35	52.2	21	10	US-09-864-761-47985	
15	34	50.7	98	σ	US-09-738-626-5715	Sequence 5715, Ap
16	34	50.7	95	10	US-09-764-864-1031	Sequence 1031, Ap
17	34	50.7	338	σ	US-09-978-295A-119	Sequence 119, App
18	34	50.7	338	σ	US-09-978-697-119	Sequence 119, App
19	34	50.7	338	σ	US-09-978-192A-119	_

Sequence 119, App Sequence 119, App Sequence 14, Appl Sequence 6, Appli Sequence 24, Appli Sequence 30, Appli Sequence 28, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli Sequence 6, Appli Sequence 13026, Appli Seq	Sequence 26, Appl Sequence 107, App Sequence 2, Appli Sequence 36085, A Sequence 13, Appl Sequence 33, Appl
9 US-09-9832A-119 9 US-09-978-189-119 9 US-09-978-189-119 10 US-09-981-6449A-24 11 US-09-981-6449A-32 12 US-09-981-6449A-32 13 US-09-981-6449A-32 14 US-09-981-6449A-32 15 US-09-981-6449A-32 16 US-09-981-6449A-32 17 US-09-981-6449A-32 18 US-10-219-248-3 19 US-10-219-248-3 10 US-09-885-722-3 10 US-09-885-722-3 10 US-09-885-722-5 11 US-09-984-849-4 12 US-09-984-849-4 13 US-09-984-849-4 14 US-09-9815-242-13026	10 US-09-796-753-26 10 US-09-867-852-107 9 US-09-759-508B-2 10 US-09-864-761-36085 9 US-09-956-206A-13 9 US-09-735-056-33
553 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	333 1258 26926 28 31 344
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Pred. No. 1.8e-05;
0; Mismatches 1; Indels
Sequence 2, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SYENDEN
APPLICANT: APALDUR SYEINBJ (RNSSON
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-31
PRIOR FILING DATE: 1998-08-31
SOFTWARE: FRSEEQ FOR WINDERS GENERAL SOFTWARE: FRSEEQ FOR WINDERS OF SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKNAL); APPLICANT: BALDUR SVEINBJ(RNSSON)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.0%;
91.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: HOMO SAPIENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWXRNMRKVR 12
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Best Local Similarity
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US-09-798-869-20
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LENGTH: 15
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Sequence 2, Application US/10023096

Sequence 2, Application US/10023096

Patent No. US20020160941A1

GENERAL INFORMATION:

APPLICANT: Kruzel, Marian L.

APPLICANT: Gollnick, Paul D.

APPLICANT: Gollnick, Paul D.

TITLE OF INVENTION: Cloning, Expression, and Uses of Human TITLE OF INVENTION: Lactoferrin

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price, Holman & Stern

ADDRESSEE: Jacobson, Price, Holman & Stern
                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                        Score 65; DB 9; Length 2., Pred, No. 2.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20004

MEDIUM TYPE: Floppy disk
COMPUTER IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                We see the st. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT PELLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FESTEREQ for Windows Version 4.0
SEQ ID NO 20
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10505/P58185C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION UNDBER: US 08/238,445
FILING DATE: 05-WAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAWE: Player, William E.
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: 105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                         97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 393-5350
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington D.C.
Y: U.S.A.
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MOLECULE TYPE: protein
US-10-023-096-2
                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 CFÓWORNMRKVR 14
                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                             Gaps
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US-09-798-869-6
                                                             ..
Score 65; DB 9; Length 694;
Pred. No. 0.00066;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.1%; Score 57; DB 9; Length 15; 83.3%; Pred. No. 0.00044; tive 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.6%; Score 48; DB 9; Length 15; 63.6%; Pred. No. 0.016;
                                                                                                                                                                                                                                                                               GENERAL INFORMATION. US/09798869
| Publication No. US20030022821A1
| GENERAL INFORMATION. SYENDSIA
| APPLICANT: (YSTEIN REKDAL
| APPLICANT: SALDUR SVENDSEN
| APPLICANT: LARS VORLAND
| APPLICANT: LARS VORLAND
| TITLE OF INVENTION: BIOACTIVE PEPTIDES
| FILE REFERENCE: A34049-PCT-USA-A
| CURRENT APPLICATION NUMBER: US/09/798.869
| CURRENT PILING DATE: 1999-08-31
| PRIOR PILING DATE: 1999-08-31
| PRIOR FILING DATE: 1999-08-31
| PRIOR FILING DATE: 1999-08-31
| PRIOR PRIOR DATE: 1999-08-31
| PRIOR FILING DATE: 1999-08-38
| NUMBER OF SEQ ID NOS: 30
| SOFTWARE: FASELSEQ FOR WINDOWS VERSION 4.0
| SEQ ID NO SEQ ID NOS: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (VSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SSOFTWARE: FastSEQ for Windows Version 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
        97.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Seguence
  Query Match
Best Local Similarity 91.7
Matches 11, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10; Conservative
                                                                                                           1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFQWXRNMRKVR 12
                                                                                                                                                            22 CFÓWORNMRKVR 33
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Best Local Similarity
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; ORGANISM: CAPRINE
US-09-798-869-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                      APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: APLOUR SVEINBJ(RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/799,869
CURRENT PELING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-36
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FRESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 22, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                        Sequence 4, Application US/09798869; Publication No. US20030022821A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.5
Matches 6; Conservative
         1 CFQWXRNMRKV 11
                                                3 CYÓWOWRMRKL 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CFOWXRNMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: MURINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-798-869-22
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LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: synthetic peptide (modified form of homo sapiens OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.6%; Score 48; DB 9; Length 25; 63.6%; Pred. No. 0.026; tive 2; Mismatches 2; Indels
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59.7%; Score 40; DB 9; Length 15; 54.5%; Pred. No. 0.4; Live 2; Mismatches 3; Indels
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: (YSTEIN RENDAL
APPLICANT: (YSTEIN RENDAL
APPLICANT: LARS VORLAND
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
TYPE: PRIOR PRIOR FILING
                                                                                                                                                                                                                                                         APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TITLE REPERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-0227
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: GB9918938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASEURE (FOR WINDOWS VERSION 4.0
                                                                                                                                                                                               ; Sequence 23, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 7, Application US/09798869; Publication No. US20030022821A1
GENERAL INFORMATION: APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
  7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 6; Conserva
                                         1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |:|| | |||:
3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWXRNMRKV 11
                                                                                       3 CYQWQRRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: CAPRINE
US-09-798-869-23
                                                                                                                                                                          US-09-798-869-23
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  Matches
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US-09-864-761-47985
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                                       Sequence 2. Application US/0988320
Publication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: Berber', Andrea E.
APPLICANT: Miluli, Khisimuzi
APPLICANT: Miluli, Khisimuzi
APPLICANT: APPLICANT: The Government of the United States of America
APPLICANT: The Government of the United States of America
APPLICANT: Department of Health and Human Services
TITLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REFERENCE: 015280-413100US
CURRENT APPLICATION NUMBER: US/09/888,320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: wild-type EtaA monooxygenase (Rv3854c, EthA)
US-09-888-320-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: SYNTHETIC PEPTIDE (modified form of caprine OTHER INFORMATION: sequence)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55.2%; Score 37; DB 9; Length 489; 54.5%; Pred. No. 36; 3; Indels trive 2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53.7%; Score 36; DB 9; Length 15; 54.5%; Pred. No. 2; tive 1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: (YSTEIN RENDAL
APPLICANT: (YSTEIN RENDAL
APPLICANT: LARS VORLAND
APPLICANT: ADALORS VORLAND
TILLE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798.869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/214,187
PRIOR FILING DATE: 2000-06-26
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 54.2
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWXRNMRKV 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 489
RESULT 10
US-09-888-320-2
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RESULT 12
US-09-798-869-29
Sequence 29, Application US/09798869
Sequence 29, Application US/09798869
Sequence 29, Application US/09798869
Sequence 29, Application US/09798869
SEQUENCE 20, APPLICANT: US/0978869
APPLICANT: HOWN SIGURD SVENDSEN
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
LEENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: GYSTEIN REKDAL
APPLICANT: SHALDUR SVEINBJ (RNSSON
APPLICANT: BALDUR SVEINBJ (RNSSON
TITLE OF INVENTION: BIOGETIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
STOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SEQ ID NO 30
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-798-869-30
; Sequence 30, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
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45.5%;
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Best Local Similarity
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Best Local Similarity
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US-09-798-869-30
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FILE REFERENCE: 249-125
CURRENT APPLICATION: NOVEL POLYNUCLEOTIDES
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: UP 99/377484
PRIOR PILING DATE: 1999-12-16
PRIOR PILING DATE: 1999-12-16
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALCHING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALCHING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: PALCHING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Corynebacterium glutamicum
                               MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 45.5%;
Matches 5; Conservative
                                                                                           HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                       OZAKI, AKIO
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73 FEYRRQLRKIR 83
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Rank, David R.
APPLICANT: Gran, Warnhead
TITLE OF INVENTION: URBER: 19/09/864,761
CURRENT PAPLICATION NUMBER: US/09/864,761
RRIOR APPLICATION NUMBER: US/09/864,761
RRIOR APPLICATION NUMBER: US/09/862,366
RRIOR APPLICATION NUMBER: US/09/862,366
RRIOR APPLICATION NUMBER: US/09/863,359
RRIOR APPLICATION NUMBER: US/09/864
RRIOR APPLICATION NUMBER: US/09/866
RRIOR APPLICATION NUMBER: US/09/866
RRIOR APPLICATION NUMBER: US/09/866
RRIOR APPLICATION NUMBER: PT/09/10/866
RRIOR APPLICATION NUMBER: PT/09/10/80/80
RRIOR FILING DATE: 2001-01-30
RRIOR PLING DATE: 2001-01-30
RRIOR PRING DATE: 2001-01-30
RRIOR PLING DATE: 2001-01-30
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OTHER INFORMATION: MAP TO AL096701.14

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6

SOUTH OF THE INFORMATION: EST_HUMAN HIT: AW294800.1, EVALUE 1.00e-06
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SEQ ID NO 47985
LENGTH: 21
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Best Local Similarity 83.3%;
Matches 5; Conservative
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ORGANISM: Homo sapiens
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Gaps 0;

1; Indels

0; Mismatches

RESULT 15
US-09-738-626-5715
Sequence 5715, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:

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                                    Gaps
                                      .
0
Score 34; DB 9; Length 86;
Pred. No. 23;
4; Mismatches 2; Indels
                                                                                                                                                          Search completed: February 21, 2003, 08:11:55 Job time: 7.88372 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec

US-09-743-107B-87 67 1 CFQWXRNMRKVR 12 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 73:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

hypothetical prote	RNA 1a protein - b	phytochrome C - so	pyruvate carboxyla	pyruvate carboxyla	probable helicase	trichohyalin like	resistance protein	protein UNC-89 - C	vif protein - simi	hypothetical prote	arginyltransferase	signal peptidase I	33.3K hypothetical	conserved hypothet	hypothetical prote
T28820	P1BVBB	T14803	C97686	AE2911	T41378	B85431	T30563	T29757	807989	D89836	AI3401	E87515	G86403	C82234	T33211
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932	996	1135	1174	1174	1213	1432	1804	6642	214	224	249	255	289	323	335
52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	52.2	50.7	50.7	50.7	50.7	50.7	50.7	50.7
35	32	35	32	32	32	32	35	35	34	34	34	34	34	34	34
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

TEHUL
lactotransferrin precursor [validated] - human
N'Alternate names: lactoferrin
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change 08-Dec-2000
C,Accession: G01394; S11228; A45401; S10324; S15853; S20841; S07160; A61169; A31000;
R,Cho, Y.
submitted to the EMBL Data Library, March 1994
A;Reference number: G06820
A;Accession: G01394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: mRNA
A, Residues: 1-711 <cho></cho>
A; Cross-references: EMBL: U07643; NID: 9467236; PIDN: AAB60324.1; PID: 9467237
R, Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R.
Nucleic Acids Res. 18, 5288, 1990
A, Title: Complete nucleotide sequence of human mammary gland lactoferrin.
A; Reference number: S11228; MUID: 90384839; PMID: 2402455
A;Accession: S11228
A; Molecule type: mRNA
A;Residues: 1-148,'T',150-422,'C',424-711 <rey></rey>
A Change and Control of the Control

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A;Cross-references: EMBL:X53961, NID:g34415; PIDN:CAA37914.1; PID:g34416
R;Teng, C.T.; Liu, Y.; Yang, N.; Walmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A;Title: Differential molecular mechanism of the estrogen action that regulates lactofer A;Reference number: A45401; MUID:93125571; PMID:1480183

A, Accession: A44501
A, Molecule type: DNA
A, Residues: 1-15 - CEN>
A, Residues: 1-15 - CEN>
A, Experimental source: placenta
A, Experimental source: placenta
A, Note: sequence extracted from NCBI backbone (NCBIP:122202)
B, Powell, M.J.; Ogden, J.E.
Nucleic Acids Res. 18, 4013, 1990
A, Fitle: Nucleotide sequence of human lactoferrin cDNA.
A, Reference number: S10324; MUID:90326549; PMID:2374734

A; Accession: S10324

A; Molecule type: mRNA A; Residues: 3-711 < POW>

A,Cross-references: EMBL:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R;Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A;Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A;Reference number: S15853; MUID:91264786; PMID:2049066

A; Status: nucleic acid sequence not shown; not compared with conceptual translation A; Molecule type: mRNA A; Residues: 20-31 <ST1> A; Accession: S15853

A; Accession: S20841

A;Molecule type: protein A;Residues: 20-28,'X',30-31 <ST2>

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71.6%;
63.6%;
   Query Match
Best Local Similarity 63.5-
'...a 7; Conservative
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A Molecule type: protein
A Residues: 1-33 <QIA>
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Matches 6, Conserva
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19 CYOWOKKOMRKL 29
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A; Residues: 436-487, 74, 489-711 < RAD>
A; Cross-references: EMBL: M18642; NID: 9186815; PIDN: AAA86665.1; PID: 9386855
A; Panella, T.J.; Liu, Y.; Liu, Y.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 3-701, 'SWKDVN' <PAN>
A; Residues: 3-701, 'SWCDVN' <PAN>
A; Residues: A: 1.5 'Source: normal breast tissue
B; Retz-Boutigue, M.H.; Jolles, J; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.;
Bur. J. Biochem. 145, 659-666, 1984
A; Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth
A; Reference number: A31000; MUID: 85076667; PMID: 6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: protein

A; Mesidues: 20-140,142-1169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4

A; Nestes: 15 the final paper in a series

R; Houen, G.; Hoegdall, E.V.; Barkholt, V.; Norskov, L.

B; Houen, G.; Jacochen. 241, 303-308, 1996

A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin

A; Reference number: S74119; MUID:97054624; PMID:8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Keywords: duplication; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SiG>
F;2-10-10/Product: lactotransferrin #status experimental <WAT>
F;21-356/Domain: transferrin repeat homology <TRH1>
F;36-699/Domain: transferrin repeat homology <TRH2>
F;39-65,39-56,135-218,177-193,190-201,251-265,503-697,595-609/Disulfide bonds: #status e
F;157-498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
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Rile Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A; Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant lo A; Reference number: UC2323; MUID:94380047; PMID:8093048
A; Recession: UC2323; MUID:94380047; PMID:8093048
A; Rocession: UC2323
A; Molecule type: mRNA
A; Residues: 1-708 < LEP>
C; Superfamily: transferrin; transferrin repeat homology
C; Superfamily: transferrin; plycoprotein
F; 359-696/Domain: transferrin repeat homology < TRH2>
F; 359-696/Domain: transferrin repeat homology < TRH2>
F; 252, 300, 387, 495, 564/Binding site: carbohydrate (Asn) (covalent) #status predicted
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 398-959, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression
A;Reference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ô
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C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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91.7%; Pred. No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A61169; MUID: 91235214; PMID: 1674448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 3q21-3q23
C;Superfamily: transferrin; transferrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GDB:119368; OMIM:150210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFOWORNMRKVR 50
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A61169
                                                                                                                               A; Accession: S07160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: GDB:LTF
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hypothetical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C;Accession: AB0858
R;Parkhili J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
A;Muthors S.; O'Gaora, P.
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Hile: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
Biochim. Biophys. Acta 1243, 25-32, 1995
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: S52107; MUID:95127729; PMID:7827104
A;Accession: S52107
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
C;Accession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                          lactoferrin - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Length 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67.2%; Score 45; DB 2; Length 33; 54.5%; Pred. No. 0.12;
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                                                                            2; Indels
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C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. 9.1;
0; Mismatches
                                                                            2; Mismatches
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   Score 48;
Pred. No.
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Best Loca Matches

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C;Accession: T08030
R;Mitchell, D.R.; Brown, K.S.
A;Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: 216302; MUID:94274778; PMID:8006077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ajnirons: 48/2; 74/3; 105/3; 159/1; 225/3; 358/3; 514/3; 729/2; 919/3; 1004/3; 1115/3; 3334/3; 3686/3; 3882/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nucleotide binding; P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
........ sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;AReference number: A84420; MUID:20083487; PMID:10617197
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A;Residues: EMBL:Z35602; PIDN:CAA84671.1; GSPDB:GN00021; CESP:R13G10.2
                                                                                                                                                                                                           A;Cross-references: GB:AE002093; NID:g4586022; PIDN:AAD25641.1; GSPDB:GN00139
C;Gentatics:
A;Gene: At2g05650
A;Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein R13G10.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T24218
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C;Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
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A;Residues: 1-4568 <MIT>
A;Cross-references: EMBL:U02963; NID:g409965; PIDN:AAA19956.1; PID:g514215
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                                                                                                                                                                                                                                                                                                                                                                   DB 2;
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                                                                                                                                                                                                                                                                                                                                                                Score 38; DB Pred. No. 34; 1; Mismatches
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A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                56.7%;
75.0%;
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A,Map position: 3
A,Introns: 64/3; 194/1; 404/3
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Matches 6; Conservative
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Best Local Similarity
                                                                                                                                                                                   A; Residues: 1-531 <STO>
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                                                                                                                        A, Status: preliminary A, Molecule type: DNA
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A, Map position: IX
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Nathernate names: lactoferrin

Shalternate names: lactortransferrin

Arritle: Lactortransferrin is the major estrogen inducible protein of mouse uterine secre
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K;Lin, X.; Kaul, S.; Rounaley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
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A,Residues: 3-707 V-PEN>
A,Schaidues: 3-707 V-PEN>
A,Cross-references: EMBL: 303298
R;Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A;Fitle: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205, MUID:92042099; PMID:1939212
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb_2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
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C;Keywords: duplication; glycoprotein
F;I-19/Domain: signal sequence #status predicted <SIG>
F:20-707/Product: lactotransferrin ferrin #status predicted <MAT>
F;358-695/Domain: transferrin repeat homology <TRH2>
F;494/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                      A,Map position: X
A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58.2%; Score 39; DB 2; Length 275; 63.6%; Pred. No. 12; tive 1; Mismatches 3; Indels
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                                                                                                                                                    A;Status: preliminary; translated from GB/EMBL/DDBJ
                           R,Dobson, R. submitted to the EMBL Data Library, October 1996 A;Reference number: Z19587 A;Recession: T22597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 63.6%;
les 7; Conservative
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A;Molecule type: DNA
A;Residues: 1-15 <LIU>
A;Cross-references: GB:M74778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 FOWKISMRKTR 272
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A; Residues: 1-275 <WIL>
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Best Loca Matches

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Gaps

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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonsc Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. Mature 408; Hughes, B.; Huizar, L. Alansen, N.F.; Hughes, B.; Huizar, L. Alansen, C.S.; Khan, S.; Khaykin, E.; Kim, C. A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A.; Luros, J.S.; Maiti, R.; Marziali A.; Rooney, T.; Rowley, D.; Sakano, H. D.; Sun, H.; Tallon, Rer, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A.; Sun, H.; Tallon, A;Reference and analysis of Chromosome 1 of the plant Arabidopsis. A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Halobacterium sp. NRC-1
C;Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 02-Peb-2001
C;Accession: C84325
K;Ngy, W. V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, i. Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabl Jung, K.H.; Alam, M.; Freitas, T.
Jung, K.H.; Alam, M.; Freitas, T.
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; I. A;Althe: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016550
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999 C;Accession: T39801
R,McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M. submitted to the EMBL Data Library, July 1999
A,Reference number: Z21880
A,Accession: T39801
A,Status: preliminary; translated from GB/EMBL/DDBJ
A,Ncleaule type: DNA
A,Rolecule type: DNA
A,Residues: 1-501 < MCD>
A,COSB-references: EMBL:AL109731; PIDN:CAB52037.1; GSPDB:GN00067; SPDB:SPBC19C2.10
A,Experimental source: strain 972h-; cosmid c19C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE004437; NID:g10581192; PIDN:AAG19967.1; GSPDB:GN00138
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fi5il.22 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C96582
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.2%; Score 37; DB 2; Length 501; 60.0%; Pred. No. 48; ive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37; DB 2; Length 584;
Pred. No. 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 55.2%;
Best Local Similarity 41.7%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 CPTWRKDMERKR 456
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A;Molecule type: DNA
A;Residues: 1-584 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Introns: 196/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 07-Oct-1994
C;Accession: B60950
R;Law, A.; Scott.
J; 109-1120, 1990
A;Title: A cross-species comparison of the apolipoprotein B domain that binds to the LDI
A;Reference number: A60950; MUID:90324804; PMID:2373961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Note: authors translated the codon ATA for residue 8 as Val
C,Superfamily: apolipoprotein B
C,Keywords: atherosclerosis; calcium; cholesterol metabolism; chylomicron; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probable monooxygenase - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: Mycobacterium tuberculosis
C;Species: T.7ull-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: C70655
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S;Conor, R.; Davies, R.; Peulwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S. Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Authors: C70655
A;Accession: C70655
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A;Accession: C70655
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A;Accession: C70655
A;Accession: DAA
A;Accession: C70655

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A;Cross-references: GB:283864; GB:AL123456; NID:G3261687; PIDN:CAB06212.1; PID:e301250;
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hypothetical sh3-containing protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
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                                                                                                                                                                Length 4568;
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                                                                                                                                                                                                                                                 4; Indels
                                          F;2202-2209/Region: nucleotide-binding motif A (P-loop)
F;2530-2537/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                Score 38; DB 2; I
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    apolipoprotein B-100 - rat (fragment)
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                                                                                                                                                                56.7%;
                                                                                                                                                                                                                                                 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             1852 CPÓWQSQLRYIQ 1863
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Matches 6; Conserv
                                                                                                                                                                     Query Match
Best Local Similarity
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A; Residues: 1-274 < LAW>
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C70655
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A;Status: preliminary

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A;Molecule type: DNA
A;Residues: 1-124 <STO>
A;Cross-references: GB:AE005173; NID:g4587555; PIDN:AAD25786.1; GSPDB:GN00141
C;Genetics:
A;Gene: F1511.22
A;Map position: 1
                                                                                                                                                                                                         0; Gaps
                                                                                                                                                         Query Match 53.7%; Score 36; DB 2; Length 124; Best Local Similarity 50.0%; Pred. No. 19; Matches 5; Conservative 3; Mismatches 2; Indels
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A; Molecule type: DNA A; Residues: 1-298 «KUR.)
A; Residues: 1-298 «KUR.)
A; Residues: 1-298 «KUR.)
A; Residues: 1-298 «KUR.)
A; Residues: 1-298 «KUR.) hypothetical protein alr4323 [imported] - Nostoc sp. (strain PCC 7120)

Query Match 53.7%; Score 36; DB 2; Length 298; Best Local Similarity 66.7%; Pred. No. 45; Matches 6; Conservative 0; Mismatches 3; Indels A;Gene: alr4323

0;

0; Gaps

Search completed: February 21, 2003, 08:02:43 Job time : 11.6047 secs

us-09-743-107b-87.rsp

Page 1

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:28:06; Search time 5.2093 Seconds (without alignments) 95.544 Million cell updates/sec

US-09-743-107B-87 67 Title: Perfect score: Sequence:

1 CFQWXRNMRKVR 12

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIMMARIES

į	ж° ,			SUMMARIES	
Score	Query Match	Query Match Length	DB	ID	riptio
65	97.0	711	न	TRFL HUMAN	P02788 homo sapien
48	71.6	708	Н	TRFL CAMDR	camel
48	71.6	708	Н	TRFL CAPHI	Q29477 capra hircu
40	σ	292	Н	NLA DROME	Q9xzl8 drosophila
40	59.7	695	Н	TRFL HORSE	
39	58.2	707	Н	TRFL MOUSE	_
38	56.7	146	Н	RPOB_LIBAF	
38	Ŋ	783	Н	YNR2 CAEEL	
38		456	Н	DYHB CHLRE	Q39565 chlamydomon
36			Н	1A34 HUMAN	
36		36	Н	SPI1 MYXVL	шухоп
36		42	Н	SYH CHLMU	Q9pjj9 chlamydia m
36		749	Н	VP4_ROTGA	
35			Н	RL28 THETN	
35			~	VIA BBMV	
35	52.2	-	٦	PHYC SORBI	P93528 sorghum bic
34			Н	VIF SIVS4	
34			Н	PAFA CHICK	
34			Н	SYH CHLTR	ਹ
34	50.7		7	SYH CHLPN	
34	50.7		Н	YKYL CABEL	
34	50.7		Н	YQS1 CAEEL	Q09309 caenorhabdi
34	50.7		٦	TLCE_RICPR	005962 rickettsia
34	50.7		Н	COR1_SCHPO	O13688 schizosacch
34	50.7		Н	PDI1 HUMAN	рошо
34	50.7		Н	Y008 HUMAN	3 homo
34	50.7		Н	T100 HUMAN	homo
34	50.7	1202	Н	JAG2_RAT	rattr
34	50.	1238	Н	JAG2 HUMAN	Q9y219 homo sapien
34		1247	۲	JAG2 MOUSE	mus n
34	。	2151	Н	RRPL_SEOU8	P27314 secul virus
34	50.7	4568	Н	DYHC_CAEEL	ā
33.5	50.0	727	Н	KDGA RAT	P51556 rattus norv

088673 mus musculu Q99up4 staphylococ	P16903 ovine lenti Q58118 methanococc	P32174 escherichia P46421 arabidopsis	O9kdle bacillus ha	USS18S Synechocyst P16710 vaccinia vi	P20993 vaccinia vi	P26929 lactobacill	095125 homo sapien
KDGA MOUSE RL28_STAAM	REV OMVVS Y708 METJA	FDOI_ECOLI GTXA_ARATH	CCDA_BACHD	Y495_SYNY3 VA16_VACCV	VA16_VACCC	URE1 LACFE	Z202_HUMAN
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730	144	211	238	246 275	378	573	648
50.0	49.3 49.3	49.3	49.3	49.3 89.3	49.3	49.3	49.3
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3.4 3.5	36 37	8 6 6 7	40	4 4 7 7	43	44	45

ALIGNMENTS

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PDB; 1
PDB; 1
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PDB;
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PDB;
PDB;
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     Desilva U.,
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Anderson B.F., Baker H.M., Norris G.E., Rice D.W., Baker E.N.;
"Structure of human lactoferrin: crystallographic structure analysis and refinement at 2.8-A resolution.";
J. Mol. Biol. 209:711-734(1989).
                                                                                                                                                                                                                                  The present state of the human lactotransferrin sequence. Study and alignment of the cyanogen bromide fragments and characterization of N- and C-terminal domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 237-711 FROM N.A.

McCombie W.R., Wilson R., Chen E., Gibbs R., Zuo L., Johnson D.,
Nhan M., Parnell L., Dedhia N., Ansari A., Mardis E., Schutz K.,
Gnoj L., la Bastide M., Kaplan N., Greco T., Touchman J., Muzny D.,
Chen C.N., Evans C., Fitzgerald M., See L.H., Tang M., Porcel B.M.,
Dragan Y., Giacalone J., Pae A., Powell E., Solinsky K.A., Desilva U
Diaz Perez S., Zhou X., Yu Y., Watanabe M., Doggett N., Garcia D.,
Sagripanti J.L.,
                                                                                                                                                                                                 MEDLINE=82046817; PubMed=6794640;
Metz-Boutigue M.-H., Mazurier J., Jolles J., Spik G., Montreuil J.,
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                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 436-711 FROM N.A.
MEDLINE=88001031, PubMed:3477300;
Rado T.A., Weil X., Benz E.J. Jr.;
"Isolation of lactoferrin cDNA from a human myeloid library and expression of mRNA during normal and leukemic myelopoiesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mutagenesis of the histidine ligand in human lactoferrin: iron
                                                                                   SEQUENCE OF 20-711.
MEDLINE-85076667; PubMed-6510420;
Metz-Boutigue M.-H., Jolles J., Mazurier J., Schoentgen F.,
Legrand D., Spik G., Montreuil J., Jolles P.;
"Human lactotransferrin: amino acid sequence and structural
comparisons with other transferrins.";
                                                                                                                                                                                       PRELIMINARY SEQUENCE OF 20-73; 134-171; 257-278 AND 347-530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding properties and crystal structure of the histidine-253-->methionine mutant.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haridas M., Anderson B.F., Baker B.N.; "Structure of human diferric lactoferrin refined at 2.2-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                       Jolles P.;
An 88 amino acid long C-terminal sequence of human
                        MEDLINE=90326549; PubMed=2374734;
Powell M.J., Ogden J.E.;
"Nucleotide sequence of human lactoferrin cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS) OF 20-353
MEDLINE=97156796; PubMed=9003186;
                                                                                                                                                                                                                                                                         Biochim. Biophys. Acta 670:243-254(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
MEDLINE=99190892; PubMed=10089347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Acta Crystallogr. D 51:629-646(1995).
                                                               Nucleic Acids Res. 18:4013-4013(1990)
                                                                                                                                                              J. Biochem. 145:659-666(1984).
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                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 142:107-110(1982).
SEQUENCE OF 3-711 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blood 70:989-993(1987).
               TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                  SEQUENCE OF 609-711
                                                                                                                                                                                                                                                                                                                                                              lactotransferrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING OF AN ANION, USUALLY BICARBONATE.
FUNCTION: LACTOFERROXINS A, B AND C HAVE OPIOID ANTAGONIST ACTIVITY. LACTOFERROXIN A SHOWS PREFERENCE FOR MU-RECEPPORS, WHILE IACTOFERROXIN B AND C HAVE SOMEWHAT HIGHER DEGREES OF PREFERENCE FOR KAPPA-RECEPTORS THAN FOR MU-RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                CHARACTERIZATION OF LACTOFERROXINS.
MEDLINE-911.66929; PubMed=136923;
Tani F., Io K., Chiba H. Yoshikawa M.;
"Isolation and characterization of opioid antagonist peptides derived
Sun X.L., Baker H.M., Shewry S.C., Jameson G.B., Baker E.N.; "Structure of recombinant human lactoferrin expressed in Aspergillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klintworth G.K., Sommer J.R., Obrian G., Han L., Ahmed M.N., Qumeisyeh M.B., Lin P.-Y., Basti S., Reddy M.K., Kanai A., Hotta Y., Sugar J., Kumaramanickavel G., Munier F., Schorderet D.F., Hotta L. Hejtmancik J.F., Teng C.T., Fasier-Kupfer M., Nagata M., Nakayasu K., Hejtmancik J.F., Teng C.T., Teng C.T., Residential subpetitehalal corneal amyloidosis (gelatinous drop-like corneal dystrophy): exclusion of linkage to lactoferrin gene."; Mol. Vision 4:31-32 (1998)
                                                                                                                                                                                                                                                    Jameson G.B., Anderson B.F., Norris G.B., Thomas D.H., Baker E.N., "Structure of human apolactoferrin at 2.0-A resolution. Refinement and analysis of ligand-induced conformational change.";
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-i- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DCMAINS.
-i- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Agric. Biol. Chem. 54:1803-1810(1990).
                                                                                                                                                                                                                                                                                                                                                                    Acta Crystallogr. D 54:1319-1335(1998)
                                                                                                            Acta Crystallogr. D 55:403-407(1999).
                                                                                                                                                                                                                         MEDLINE=99192677; PubMed=10089508;
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XS2941; CAA37116.1; -.
U95626; AAB57795.1; -.
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M83205; AAA58656.1; -.
M18642; AAA86665.1; -.
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1LCT; 31-OCT-93.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Mammary gland;
Paramasivam M., Srinivasan A., Singh R., Sahani M.S., Singh T.P.;
Submitted (UUN-1999) to the EMBL/Genbank/DDBJ databases.
-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSFORP PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                            Gaps
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Mammalia, Butheria, Cetartiodactyla, Tylopoda, Camelidae, Camelus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=Somali; TISSUE=Lactating mammary gland;
Kappeler S.R., Ackermann M., Farah Z., Puhan Z.;
"Sequence analysis of camel (Camelus dromedarius) lactoferrin.";
Int. Dairy J. 9:481-486(1999).
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PRINTS; PR00422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                         6,
  97.0%; Score 65; DB 1; Length 711; 91.7%; Pred. No. 0.00015; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Camelus dromedarius (Dromedary) (Arabian camel).
                                                                                                                                                                                                                                                                                    TRFL_CAMDR STANDARD; PRT; 708 AA. Q9TUMO; Q9YES5; 16-0CT-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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EMBL; AF165879; AAF82241.1; -...
HSSP; O77811; 1BIX.
InterPro; IPR001156; Transferrin.
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IRON 1 (BY SIMILARITY).
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IRON 2 (BY SIMILARITY).
IN-LINKED (GLUNC. ...) (POTENTIAL).
IN-LINKED (GLUNC. ...) (POTENTIAL).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Caprinae; Capra.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.6%; Score 48; DB 1; Length 708; 66.7%; Pred. No. 0.21; ive 1; Mismatches 3; Indels
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TISSTE-Mammary gland;
Lee T. Yu S., Kim S., Lee K., Yu D.,
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TRFL_CAPHI STANDARD; PRT; 708 AA. 029477; 029479; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1002 (Rel. 37, Last sequence update) 15-UW-2002 (Rel. 41, Last annotation update) Lactotransferrin precursor (Lactoferrin).
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708 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=9925;
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     DISULFID
                                       DISULFID
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BINDING
CARBOHYD
                                                                                                                                DISULFID
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MIA_DROME STANDARD; PRT; 292 AA. 09XZIG; 094731; Created)
30-MAY-2000 (Rel. 39, Created)
30-MAY-2001 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Nebula protein.

```
NLA DROME
                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       () (POTENTIAL).
() (POTENTIAL).
() (POTENTIAL).
() (POTENTIAL).
() (POTENTIAL).
                                                                                                                                                                                                  !ransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.6%; Score 48; DB 1; Length 708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F2EDA3C83539960D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GLCNAC...)
(GLCNAC...)
(GLCNAC...)
(GLCNAC...)
DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS. SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
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- N (IN REF. 2).

2 - N (IN REF. 2).

5 - P (IN REF. 2).

5 - N (IN REF. 2).

5 - O (IN REF. 2).
                                                                                                                                                                                                                            LACTOTRANSFERRIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 0.21;
; Mismatches
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BY SIMILARITY.
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N-LINKED
I -> V (IN
L -> R (II
Y -> P (II
S -> P (II
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N-LINKED
                                                                                                                                       PEGM, PF00405, transferrin, 2.
PRINTS, PR00422, TRANSFERRIN.
SMART; SM00094, TR. FER, 2.
PROSITE; PS00205, TRANSFERRIN 1; 2.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 2; 2.
                                                                                                                                InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77358 MW;
                                                                                                    EMBL; U53857; AAA97958.1; -. EMBL; X78902; CAA55517.1; -. HSSP; O77698; ICE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.6%;
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Matches
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RK STWAIN=Serkeley;

RAMAIN=Serkeley;

RAMAIN=Serkeley;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Holt R.A., Evans C.A., Galle R.F.;

RA Amanatides P.G., Scherer S.E., I. N., Hoskins R.A., Galle R.F.;

RA HILD G.G., Wortman J.R., Yandlall M.D., Zhang O., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,

RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.M., Banns P.V., Berman B.P., Bhandari D., Bolahakov S.,

RA Berson K.Y. Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,

RA Borkova D., Botcher A., Deng Z., Mays A.D., Doulankov S.,

RA Durbin K.J., Evangelista C. D., Broketein P., Brottler P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Durbin K.J., Boungelista C.C., Ferraz C., Ferriera S., Pleischman W.,

RA Glodek A., Gong F., Gorrell J.H.G. Z., Gelbart W.M., Glasser K.,

RA Hostin D., Houston K.A., Howland T.J., Mernandez J.R., Houck J.,

RA Alali M., Kalush F., Kalpen G.H., Ke Z., Kulp D., Lai Z.,

RA Alali M., Kalush F., Rapen G.H., Ke Z., Kulp D., Lai Z.,

RA Martei B., Modintoh T.C., McLeod M.P., Moshrefi A.,

RA Martei B., Morintoh T.C., McLeod M.P., Noshrefi A.,

RA Shue B., Dela-Kiamos I. Simpson M., Strong R., Sun F.,

RA Shue B., Sordari R.A., Nixon K., Nusskern D.S., Purk, Noshrefi A.,

RA Shue B., Spradling A.C., Stapleton M., Strong R., Sun F.,

RA Shue B.C., Siden-Kiamos I. Simpson M., Strong R., Sun E.,

RA Shue B.C., Stand-Kiamos I. Simpson M., Strong R., Sun E.,

RA Shue B., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Shue B.C., Stand-Kiamos I. Stapleton M., Strong R., Sun K.,

RA Shue B.C., Stand-Kiamos I. Stapleton M., Strong R., Sun K.,

RA Shue B.C., Stand-Kiamos I. Stapleton M., Strong R., Sun E.,

RA Shue B.C., Stand-Kiamos I. Stapleton M., Strong R., Sun E.,

RA Shue B.C., Stand-Kiamos I. Stapleton M., Strong R., Sun K.,

RA Shue B.C., Stand-Kiamos I. Stapleton M., Strong R., Sun E.,

RA Shue B.C., Stand-Kiamos I., St
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                                    Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
McCormick A.V., Goldberg M.L.;
"Gene required for elongation of meiosis I spindle in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- FUNCTION: REQUIRED FOR ELONGATION OF MEIOSIS I SPINDLE -!- SIMILARITY: BELONGS TO THE DSCRI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-Berkeley;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            females.
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Gaps

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7; Conservative

1 CFQWXRNMRKV 11 CYQWQRRMRKL 48

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38

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Strausberg R.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Biol. 289:303-317(1999).
-!- FUNCTION: TRANSFORINS ARE IRON BINDING TRANSFORT PROTEINS WHICH
CAN BIND TWO ATOMS OF FERRIC IRON IN ASSOCIATION WITH THE BINDING
OF AN ANION, USUALLY BICARBONATE.
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sharma A.K., Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P., "Three-dimensional structure of mare diferric lactoferrin at 2.6-A resolution.";
                                                                                                                                                                                                                                                                                                                 Būkaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
NCBI_TaxID=9796;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1422; TRANSFERIN,
SMART; SM00094; TR FER; 2.
PROSTIE; PS00205; TRANSFERIN 1; 2.
PROSTIE; PS00206; TRANSFERIN 2; 2.
PROSITE; PS00207; TRANSFERIN 2; 2.
Transport; Iron transport; Glycoprotein; Metal-binding; Repeat;
                                                                                                               .
0
                                                                                   59.7%; Score 40; DB 1; Length 292; 54.5%; Pred. No. 2.6; ive 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Paramasivam M., Srinivasan A., Yadav M.P., Singh T.P.,
"CDNA sequence of mare lactoferrin.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                     EMBL; AR147700; AAD33987.1; -.
EMBL, AB003712; AAF55285.1; -.
FYPase; FBGN0026629; nla.
SEQUENCE 292 AA; 31423 MW; 64F1BBF5F6EA6CF9 CRC64;
                                                                                                                                                                                                                                            15-UUL-1999 (Rel. 38, Created)
15-UUL-1999 (Rel. 38, Last sequence update)
15-UUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  - SUBCELLULAR LOCATION: Secreted.
- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                         695 AA.
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99296631; PubMed=10366507;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001156; Transferrin.
Pfam; PF00405; transferrin; 2.
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                                                                                                            Conservative
                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                           Equus caballus (Horse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 181X; 02-DEC-98.
PDB; 187U; 02-FEB-99.
PDB; 187Z; 02-FEB-99.
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NON TER 1
SIGNAL <1
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150 FQWLRSFRRLR 160
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                                                                                                                                   2 FOWXRNMRKVR 12
                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                      TRFL HORSE
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                                                                                                          Matches
                                                                                                                                                                                              RESULT 5
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SLWILLE.

(GLCNAC. .) (FOIDM.

(GLCNAC. .) (POTENTIAL)

(POTENTIAL)
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moriishi K.;
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07BB84D50E1B165D CRC64;
                                                                                                                                                                                                                                                                                                           IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
ANION (BY SIMILARITY).
N-LINKED (GLCNAC. . .)
N-LINKED (GLCNAC. . .)
LACTOTRANSFERRIN.
1.
2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P08071; P70690; Q61799; Q922P2;
01-AUG-1988 (Rel. 08, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lactotransferrin precursor (Lactoferrin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   uterine secretions.";
J. Biol. Chem. 262:10134-10139(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Uterus;
MEDLINE=87280033; Pubmed=3611056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75991 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CFQWXRNMRKVR 12
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CAKFORNMKKVR 36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695 AA;
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198
4401
6601
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169
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                                    REPEAT
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TRFL_MOUSE
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CONFLICT
CONFLICT
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CONFLICT
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                                                                                                                 Query Match
CONFLICT
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                                                                                                                                                                                                                                                                     RESULT 7
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STEETS
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                                                                Liu Y., Teng C.T.;

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

"Characterization of estrogen-responsive mouse lactoferrin promoter.";

J. Biol. Chem. 266:21880-21885(1991)

-!- FUNCTION: TRANSFERRINS ARE IRON BINDING TRANSPORT PROTEINS WHICH

CAN BIND TWO ATOMS OF PERRIC IRON IN ASSOCIATION WITH THE BINDING

OF AN ANION, USUALLY BICARBONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
MR -> 10G (IN REF. 1).
R -> Q (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                !ransport; Iron transport; Glycoprotein; Metal-binding; Repeat;
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 1 (BY SIMILARITY).
IRON 2 (BY SIMILARITY).
ANION (POTENTIAL).
                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- DOMAIN: COMPOSED OF TWO HOMOLOGOUS DOMAINS.
-!- SIMILARITY: BELONGS TO THE TRANSFERRIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
LACTOTRANSFERRIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEAM; PF00405; transferrin; 2.
PRINTS; PR0422; TRANSFERRIN.
SMART; SM00094; TR FER; 2.
PROSITE; PS00205; TRANSFERRIN 1; 1.
PROSITE; PS00206; TRANSFERRIN 2; 2.
PROSITE; PS00207; TRANSFERRIN 3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; P02788; ICB6.
MGD; MGI:96837; Ltf.
InterPro; IPR001156; Transferrin.
                                SEQUENCE OF 1-14 FROM N.A.
MEDLINE=92042099; PubMed=1939212;
                                                                                                                                                                                                                                                                                                                                                                                         EMBL; J03298; AAA40525.1; -.
EMBL; D88110; BAA13633.1; -.
EMBL; BCO066904; AAH06904.1; -.
EMBL; M74778; AAA39427.1; -.
PIR; A28438; A28438.
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-!- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Nelspruit;
Planet P., Jagoueix S., Bove J.M., Garnier M.;
"Detection and characterization of the African Citrus Greening
"Libercolater by amplification, cloning and sequencing of the rplKAJL-
rpoBC operon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-1995 (Rel. 31, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
11-NOV-2001 (Rel. 40, Last annotation update)
DNA-directed RNA polymerase beta chain (RC 2.7.7.6) (Transcriptase beta chain) (RA polymerase beta subunit) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Liberibacter africanus (Liberobacter africanum).
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Rhizobiaceae; Candidatus Liberibacter.
NCBI_TaxID=34020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA CHAIN FAMILY.
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                                                                                                                                                                                                            DB 1; Length 707;
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Interpro; IPR001572; RNA_pol_B.
PFGM; PF00562; RNA_pol_B; 1.
PROSITE; PS01166; RNA_POL_BETA; PARTIAL.
Transferae; Transcription; DNA-directed RNA polymerase.
NON_TER 146 146
                                                                                                                                                                                                                                                                      4; Indels
82 M -> L (IN REF. 2).
359 S -> T (IN REF. 2).
482 A -> D (IN REF. 1).
449 E -> G (IN REF. 2).
77865 MW; P26AB0340A4C19A8 CRC64;
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SEQUENCE 146 AA; 16731 MW; 815D6EDD66FD8943 CRC64;
                                                                                                                                                                                                         h Similarity 54.5%; Score 39; DB 1
Similarity 54.5%; Pred. No. 9.6;
6; Conservative 1; Mismatches
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            82
359
382
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629
670 AA;
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Best Local Similarity
Matches 6; Conserv
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Matches 6; Conserv
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                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Cell Sci. 107:635-644(1994).
-!- FUNCTION: FORCE GENERATING PROTEIN OF EUKARYOTIC CILIA AND FLAGELLA. PRODUCES FORCE TOWARDS THE MINUS ENDS OF MICROTUBULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mitchell D.R., Brown K.S.;
"Sequence analysis of the Chlamydomonas alpha and beta dynein heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydomonas reinhardtii.
Bukaryota, Viridiplantae, Chlorophyta, Chlorophyceae, Volvocales,
Chlamydomonadaceae, Chlamydomonas.
                                                                                                                                                                                                                                                  -!- COFACTOR: FAD (POTENTIAL).
-!- SIMILARITY: BELONGS TO THE FLAVIN MONOAMINE OXIDASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 38; DB 1; Length 783;
Pred. No. 16;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z35602; CAA84671.2; -..
WormPep; R13G10.2; CE25088.
InterPro; IPR002237; Amino oxidase.
Pfam; PF01593; Amino oxidase; 1.
Hypotherical protein; Oxidoreductase; Flavoprotein; FAD.
NP_BIND 31 366 FAD (ADP PART) (POTENITAL).
                                                                                                                                                                               Gardner A.E.;
Submitted (AUG-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                             Durbin R.;
Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       311 366 FAD (ADP PART) (POTENTIAL) 783 AA; 88799 MW; 8D087E96464DC908 CRC64;
                                           15-DEC-1998 (Rel. 37, Created)
15-UN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Hypothetical protein R13G10.2 in chromosome III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NoV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
30-MAY-2000 (Rel. 35, Last annotation update)
Dynein beta chain, flagellar outer arm.
ODA4 OR ODA-4 OR SUP1.
                        783 AA.
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                        PRT;
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MEDLINE=94274778; PubMed=8006077;
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                       STANDARD;
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Caenorhabditis elegans.
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Best Local Similarity
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                                                                                                                                   NCBI_TaxID=6239;
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                       CAEEL
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RESULT 8
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Madrigal J.A., Hildebrand W.H., Belich M.P., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
du Toit B.D., Parham P.;
"Structural diversity in the HLA-AlO family of alleles: correlations
                    -!- SUBUNIT: CONSISTS OF AT LEAST 3 HEAVY CHAINS (ALPHA, BETA AND GAMMA), 2 INTERMEDIATE CHAINS AND 8 LIGHT CHAINS.
-!- SIMILARITY: BELONGS TO THE DYNEIN HEAVY CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. (A*3401/A*3402).
MEDLINE=93056508; PubMed=1431115;
Madrigal J.A., Belich M.P., Hildebrand W.H., Benjamin R.J.,
Little A.-M., Zemmour J., Ennis P.D., Ward F.E., Petzl-Erler M.L.,
Martell R.W., du Toit E.D., Parham P.;
Distinctive HAA-A, B antigens of black populations formed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                řIA-A OR HLAA.
Homo sapiens (Human).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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P30453; P30454;
O1-APR-1993 (Rel. 25, Created)
O1-APR-1993 (Rel. 25, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
HLA class I histocompatibility antigen, AW-34 (A-10) alpha chain
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MICROTUBULE-BINDING (POTENTIAL).
COLLED COLL (POTENTIAL).
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InterPro; IPR004273; Dynein heavy.
Pfam; PF03028; Dynein heavy; 1.
Motor protein; Microtubules; Dynein; ATP-binding; Flagella;
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3; Mismatches
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DYNEIN HAS ATPASE ACTIVITY.
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1852 CFQWQSQLRYIQ 1863
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BY SIMILARITY.
BY SIMILARITY.
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                                                                                                -!- POLYMORPHISM: THE FOLLOWING ALLELES OF AW-34 ARE KNOWN: A*3401 (AW-34.1) AND A*3402 (AW34.2). THE SEQUENCE SHOWN IS THAT OF
            Tissue Antigens 41:72-80(1993).
-1- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS THE IMMUNE SYSTEM.
-1- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-MICROGLOBULIN).
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EXTRACELLULAR ALPHA-1.
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P - S (IN A*3402).

/FIId=VAR 004100
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L -> I (IN A*3402).
/FIId=VAR 004357
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/FTId=VAR 004380.
R -> I (IN A*3402).
/FTId=VAR 004381.
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/FIId=VAR 004379.
K -> N (IN A*3402).
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R (IN A*3402).
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FTId=VAR 004383.
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INTERPRO; IPR003597; Ig_cl.
InterPro; IPR001039; MHC_I.
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Pfam; PF00129; MHC I; 1.
ProDom; PD000050; MHC I; 1.
SMART; SM00407; IGc1; 1.
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with serology.";
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369 AA.

PRT;

STANDARD;

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                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91049428; PubMed=2173255;
Upton C., Macen J.L., Wishart D.S., McFadden G.;
Wyxona virus and malignant rabbit fibroma virus encode a serpin-like protein important for virus virulence.";
Virology 179:618-631(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Upton C., McFadden G.; "DNA sequence homology between the terminal inverted repeats of Shope fibroma virus and an endogenous cellular plasmid species."; Mol. Cell. Biol. 6:265-276(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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MEDLINE=20032073; PubMed=10562494;
Macaulay C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
Macaulay C., Willer D., Evans D., McFedden G.;
"The complete DNA sequence of myxoma virus.";
"The complete DNA sequence of myxoma virus.";
virology 264:299-318 [1999].
-i- FUNCTION: IMPORTANT IN VIRULENCE.
-i- SIMILARITY: BELONGS TO THE SREPHIN FAMILY. POXVIRUSES SUBFAMILY.
-i- SIMILARITY: BELONGS TO THE SREPHIN FAMILY. POXVIRUSES SUBFAMILY.
-i- CAUTION: WAS ORIGINALLY (REF. 2 AND REF. 3) THOUGHT TO ORIGINATE FROM A PLASMID RABBIT DNA. THE ORIGINAL SAMPLE WAS CONTAMINATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Serine protease inhibitor; Virulence.
3 319 320 REACTIVE BOND (BY SIMILARITY).
1 16 MKYLVLVLCLTSCACR -> MFNVVRV (IN REF. 2
                                                                                                                                                                                                            Jiruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=87030884; PubMed=3021526;
Upton C., Carrell R.W., McFadden G.;
"A novel member of the serpin superfamily is encoded on a circular plasmid-like DNA species isolated from rabbit cells.";
FEBS Lett. 207:115-120(1986).
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85.7%; Pred. No. 18;
ive 0; Mismatches 1; Indels
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01-OCT-1989 (Rel. 12, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Serine proteinase inhibitor 1 (Serpin 1) (Serp-1).
SERPI OR MOOB.1L.
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MEDLINE=87064296; PubMed=3023828;
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EMBL, M1233; AAAB1567.1; -.
EMBL, AF170726; AAF15055.1; -.
EMBL, AF170726; AAF14896.1; -.
                                                                                                                                                                              Myxoma virus (strain Lausanne)
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InterPro; IPRO00215; Serpin.
Pfam; PR00079; Gerpin; 1.
PROSITE; PS00284; SERPIN; 1.
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PIR; B36418; B36418.
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NCBI_TaxID=31530;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey B.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M., "Genome sequences of Chlamydia trachomatis Mopn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IRR002106; AAtRNA ligaseII.
InterPro; IRR004154; HGTP_anticodon.
InterPro; IRR004154; HGTP_anticodon.
InterPro; IRR002314; HRNS.
InterPro; IRR002314; HRNS.
Pfam; PRO0587; HRNA-synt 2b; 1.
Pfam; PRO0587; HGTP_anticodon; 1.
IGRRAMs; TIGR00442; hiss; 1.
PROSITE; PS50862; AA_TRNA_LIGASE_II; 1.
PROSITE; PSCOR62; AA_TRNA_LIGASE_II; 1.
PROSITE; PSCOR62; AA_TRNA_LIGASE_II; 1.
COMPLETE PROCEOME.
428 AA; 48939 MW; 9CF855EDDE689DDF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae AR39.";

Nucleic Acids Res. 28:1397-1406(2000).

-!-CATALYTIC ACITUTY: ATP + L-histidine + tRNA(His) = AMP + diphosphate + L-histidyl-tRNA(His).

-!-SUBUNIT: HOWODINER (BY SIMILARITY).

-!-SUBCELLULAR LOCATION: Cytoplasmic.

-!-SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                              16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53.7%; Score 36; DB 1; Length 428; 44.4%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2; Indels
                                                                                                                                                                                                                                                                                                          Chlamydia muridarum.
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
                                                                                                                                               428 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      749 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (
or send an email to license@isb-sib.ch)
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VP4 ROTGA STANDARD;
Q04916;
01-JUN-1994 (Rel. 29, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AE002349; AAF39630.1; -.
HSSP; O32422; 1QE0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4; Conservative
                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-MOPn / Nigg;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           348 CFSWAKHLR 356
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        NCBI TaxID=83560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CFQWXRNMR 9
                                       235 WIRNMRK 241
4 WXRNMRK 10
                                                                                                                                                                                                                                                                            (H1SKS).
HISS OR TC0830.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR; TC0830;
                                                                                                                                             SYH CHLMU
                                                                                                                                                                                                                                                                       HIBRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
VP4_ROTGA
                                                                                                                       SYH_CHLMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DAC
                                                                                                                                             HIDDEN BERNE DER PRESENTE DER PRESENTE DE PROPERTOR DE PO
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                                                                                                                                                                                                                                                                                Mackow B.R., Werner-Eckert R., Fay M.E., Tao H., Chen G.-M.; "Identification and baculovirus expression of the VP4 protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Outer capsid protein VP4 (Hemagglutinin) (Outer layer protein VP4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bao Q., Tian Y., Li W., Xu Z., Xuan Z., Hu S., Dong W., Yang J., Chen Y., Xue Y., Xu Y., Lai X., Huang L., Dong X., Ma Y., Ling L., Tan H., Chen R., Wang J., Yu J., Yang H.;
"A complete sequence of T. tengcongensis genome.";
Genome Res. 12:689-700(2002).
-! SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
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                                                                                                                Rotavirus (group B / strain ADRV) (Adult diarrhea rotavirus).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
                                                                                                                                                                                                                                                                                                                                                                       J. Virol. 67:2730-2738(1993).
-1- SUBCELLULAR LOCATION: Outer capsid.
-1- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB 1; Length 749;
Pred. No. 36;
0; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria, Firmicutes, Clostridia, Thermoanaerobacteriales, Thermoanaerobacteriaceae, Thermoanaerobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D1223527DEAE0F21 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 508 ribosomal protein L28.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-LINKED
N-LINKED
N-LINKED
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N-LINKED
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MEDLINE=21992816; PubMed=11997336;
                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE=93233240; PubMed=8386274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thermoanaerobacter tengcongensis.
                                                                                                                                                                                                                                                                                                                                            human group B rotavirus ADRV.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M91434; AAA47338.1; -.
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/anmounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dzianott A.M., Bujarski J.J.; "The nucleotide sequence and genome organization of the RNA-1 segment in two bromoviruses: broad bean mottle virus and cowpea chlorotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Virology 185:553-562(1991).
-!- FUNCTION: MAY BE INVOLVED IN THE REPLICATION OF THE VIRUS.
CONTAINS AN HELICASE DOWAIN AND A METHYLTRANSFERASE DOMAIN. THE METHYLTRANSFERASE DOMAIN IS PROBABLY INVOLVED IN VIRAL RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52.2%; Score 35; DB 1; Length 966; 46.7%; Pred. No. 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: TO 1A PROTEIN FROM CCMV, CMV, PSV AND TAV.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 35; DB 1; Length 62;
Pred. No. 4.6;
2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   966 AA; 109621 MW; DF592681D7231C8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002588; V methyltransf.
InterPro; IPR000606; Viral_helicasel.
Pfam; PF01443; Viral_helicasel; 1.
Pfam; PF01600; Vmethyltransf; 1.
Helicase; APP-binding; Transferase, Methyltransferase.
NP_BIND 690 697 ATP (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                 Ribosomal protein; Complete proteome.
SEQUENCE 62 AA; 7037 MW; CAADB605C81D495D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-UUL-1993 (Rel. 26, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
16-OCT-2001 (Rel. 40, Last amnotation update)
1A protrein [Includes: Helicase, Methyltransferase].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=92074218; PubMed=1962437;
                                                                                                                                                                                                                                                                                                                   EMBL; AE013107; AAM24713.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     52.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M65138; AAA42740.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 46.7
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Broad bean mottle virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A41699; PIBVBB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 QWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27 RWKPNIRKVR 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=12301;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mottle virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-Bawden;
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Q00020;
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4; Gaps

3; Indels

1; Mismatches

1 CFQ----WXRNMRKV 11

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347 CFKENKDWTENMRSV 361
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Search completed: February 21, 2003, 07:51:35 Job time : 6.2093 secs

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Seguence:

Run on:

Searched:

Database

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Olimg5 lumpy skin

Oghk5 yaba-like d

P9623 mycobacceri

Oghud0 schizosacch

Ogh8487 zea mays (m

Ogh943 halobacteri

Ogy446 drosophila

Ogy465 oryza sativ

Ogy401 human immun

Ogy409 human immun

Ogy409 human immun

Ogy409 human immun

Ogy117 human immun

Ogy117 human immun

Ogy117 human immun

Ogy117 human immun

Ogy118 human immun

Ogy118 human immun

Ogy118 human immun

Ogy11 carbiclephu

Ogy27 callistephu

Ogy27 callistephu
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01-MAY-2000 (TYEMBLrel. 13, Created)
01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-JUN-2001 (TYEMBLrel. 17, Last annotation update)
Lactoferrin homolog (Fragment).
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 711;
                                                                                                                                                                                                                                                                                                                                                                                                      SECURIOR PROSTATE;
Strausberg R.;
Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
SWBL; BC022347; AAH22347.1;
SEQUENCE 711 AA; 78327 MW; 1B9C7EE097C45FAF CRC64;
                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.6%; Score 60; DB 4;
90.9%; Pred. No. 0.003;
cive 0; Mismatches
                                                                                                                                                                                                                                                                                                        711 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38 AA.
                                                                                                                                                                                                                                                              ALIGNMENTS
                                      Q9D9X0
Q9JIT1
Q91MQ5
Q9DHK5
P96223
                                                                                                          Q9V346
Q9XFD5
                                                                                                                         09YQC1
09YQC0
09YQB9
09YQB8
                                                                                                                                                                                                                     Q9VI18
Q9SP27
Q9XZ30
                                                                                                                                                                  Q9YIJ2
Q8Q454
                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                      PRT;
                                                                                         085487
                                                                                                  Q9HPA3
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                                                                                                                                                                                                    OBTAX2
                                                                                                                                                                                                             Q9NUS2
2 5
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01-UUN-2002 (TrEMBLrel. 21, 0
01-UUN-2002 (TrEMBLrel. 21, 1
01-UUN-2002 (TrEMBLrel. 21, 1
Lactotransferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 90.9
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Mammalia, Euthern
NCBI_TaxID=9606;
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Q9UCYS
TO Q9UCYS
                                                                                                                                                                                                                                                                                                       Q8TCD2
                                                                                                                                                                                                                                                                                      RESULT 1
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O9u4m9 leishmania
O9fhi9 arabidopsis
O8sc55 stx2 conver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9sic0 arabidopsis
Q77855 human immun
Q77856 human immun
Q9czq7 mus musculu
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Ogucy5 homo mapien
Ogtr80 ovis mries
Omr462 malmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9xhpl sesamum ind
O31090 rhizobium l
Q93780 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                081653 hemerocalli
                                                                (without alignments)
114.078 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                      February 21, 2003, 07:44:43 ; Search time 21.6744 Seconds
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      GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 1008
Listing first 45 summaries
                                      - protein search, using sw model
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Q93780
Q8R2A4
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Q9FHI9
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Q9SIC0
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Q9XHP1
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Gapop 10.0 , Gapext 0.5
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Q9TR80
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sp_bacteria:*
sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
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Gaps

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Result 8 Ŋ

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0; Gaps

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STRAIN=TAINAN 1;
MEDLINE=20074970; PubMed=10606554;
Tai S.S.K., Wu L.S.H., Chen B.C.F., Tzen J.T.C.;
"Molecular cloning of 11S globulin and 2S albumin, the two major seed
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Krodh A., Larsen T.S., Leather S., Hien T.T., White N., Jagels K., Krodh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Hhitehead S., Barrell B.G.;

"Complete genome sequence of a multiple drug resistant Salmonella enterica servar Typhi CT18.";

Nature 413:848-852 (2001).

BMBL; ALG27276; CADG6049.1; --

Hypothetical protein; Complete proteome.

SEQUENCE 511 AA; 58126 MW; E2DDD124E10D178B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Asteridae, euasterids I; Lamiales, Pedaliaceae, Sesamum.
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01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 31.0 kDa protein.
Rhizobium leguminosarum (biovar viciae).
Bacteria, Proteobacteria; alpha subdivision, Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 41; DB 16; Length 511;
Pred. No. 9.9;
0; Mismatches 5; Indels
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InterPro; IPR000617; Napin.
InterPro; IPR001769; Try/amyl inhbtr.
Pfam; PF00234; tryp.alpha_amyl; 1.
PFININ'S; PR00499; NAPIN.
SMART; SM00499; AAI; 1.
SEQUENCE 148 AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sesamum indicum (Oriental sesame) (Gingelly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         148 AA.
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J. Agric. Food Chem. 47:4932-4938(1999).
EMBL; AF091841; AAD42943.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61.2%;
58.3%;
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Matches 7; Conservative
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Best Local Similarity
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MEDLINE=21534947; PubMed=11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ovis aries (Sheep).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
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               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Pred. No. 0.00085;
0; Mismatches 1; Indels
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SEQUENCE 38 AA: 4459 MW; 0402F490B5EBDDEB CRC64;
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Qian Z.Y., Jolles P., Migliore-Samour D., Fiat A.M.;
Biochim. Biophys. Acta 1243:25-32(1995).
HSSP; O77698; ICE2.
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Pfam; PF00405; transferrin; 1.
SEQUENCE 33 AA; 3914 MW; D1904CAE15A73961 CRC64;
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypochetical protein STX3070.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                Jpn. J. Îegal Med. 49:281-293(1995).
HSSP; P02788; 1BKA.
InterPro; IPR001156; Transferrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
                                                                                                                                                              MEDLINE=96081613; PubMed=8551695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.2%;
54.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 90.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovidae; Caprinae; Ovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lactoferrin (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 FOWXRNMRKVR 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21 FOWORNMRKVR 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 CYQWQKKMRKL 29
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SEQUENCE FROM N.A.
                                                                                                                              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                seminal plasma.";
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                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9940;
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                         SEQUENCE FROM N.A. STATE-128X1/SVJ;
STRAIN=128X1/SVJ;
MEDLINE=21676859; PubMed=11802169;
Rodriguez I., Del Punta K., Rothman A., Ishii T., Mombaerts P.;
Multiple new and isolated families within the mouse superfamily of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Buglenozoa, Kinetoplastida, Trypanosomatidae, Leishmania.
NCBI_TaxID=5664;
     Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.2%; Score 39; DB 11; Length 341; 55.6%; Pred. No. 16; 2; Indels Live 2; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.2%; Score 39; DB 5; Length 415; 66.7%; Pred. No. 20; 2; Indels iive 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Leishmania major chromosome 5 complete sequence.";
Submitted (DBC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF163772; AAF14642.1;
InterPro; IPR003409; MORN.
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE 341 AA; 39632 MW; B3D8259F7AD11130 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46701 MW; 3E3AD710BF23691E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ol-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last amotation update)
Genomic DNA, chromosome 5, Pl clone:MFC19.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      866 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                Vlr vomeronasal receptors.";
Nat. Neurosci. 5:134-140(2002).
EMBL; AY065506; AAL47911.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 55.6
Matches 5, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 66.7
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02493; MORN; 4
SEQUENCE 415 AA; 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331 CFTWTRNIK 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          272 CGEWFRINK 280
                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leishmania major.
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                                                                                                                                                                                                                                                                                                                                                                         Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea,
Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                        Sadykov M.R., Ivashina T.V., Kanapin A.A., Shlyapnikov M.G., Ksenzenko V.N.;
Ksenzenko V.N.;
"Structural and functional organization of the exopolysaccharide
biosynthesis genes in Rhizobium leguminosarum bv. viciae VF39.";
Mol. Biol. (Mosk) 32:797-804 (1998).
EMBL; AF028810; AAB88891.1;
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0
                                                                                                       Ivashina T.V., Sadykov M.R., Kanapin A.A., Ksenzenko V.N., Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59.7%; Score 40; DB 2; Length 273; 60.0%; Pred. No. 8.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Genome sequence of the nematode C.elegans: A platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.2%; Score 39; DB 5; Length 275; 63.6%; Pred. No. 13; 3; Indels iive 1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dobson R.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 273 AA; 30986 MW; F195D2FEF7AD44D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    investigating biology.";
Science 282:2012-2018(1998).
EMBL; Z81089; CAB03137.1; -.
SEQUENCE 275 AA; 31716 MW; 9D69524FFC704DB2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1997 (TrEMBLrel. 02, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                              MEDLINE=99113394; PubMed=9914965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 21, C
(TrEMBLrel. 21, L
(TrEMBLrel. 21, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vomeronasal receptor VIRE6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 63.67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 60.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
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262 FQWKISMRKTR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             245 RWLRNLRKLR 254
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                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F53H4.4 protein.
NCBI_TaxID=387;
                                                                                                                                                                                                                       STRAIN=VF39;
                                                                                   STRAIN=VF39;
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01-JUN-2002
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RESULT 7

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QBR2A4 RESULT 8 Q8R2A4

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Gaps

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Length 372; 1; Indels

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Plant Mol. Biol. 40:237-248(1999).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
EMBL; AF062028; A5424853.1; -
INTERPRO; IPR001128; Cytochrome_P450.
Pfam; PR00667; P450; 1.
PRINTS; PR00385; P450.
PRINTS; PR00386; CYTOCHROME_P450; UNKNOWN_1.
                                                                                                                         SEQUENCE 372 AA; 41909 MW; 55FB3EAF9699595E CRC64;
                                                                                                                                                     56.7%; Score 38; DB 10; 71.4%; Pred. No. 27; tive 1; Mismatches 1
                                                                                                  Heme; Moncoxygenase; Oxidoreductase.
NON TER 1 1
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Best Local Similarity
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STRAIN=CV. STELLA D'ORO; TISSUE=SENESCING PETALS;
MEDLINE=99339248; PubMed=10412903;
Panavas T., Pikula A., Reld D.D., Rubinstein B., Walker B.L.;
"Identification of senescence-associated genes from daylily petals.";
                           Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu B., Kotani H., Miyajima N., Tabata S., "Structural analysis of Arabidopsis thaliana chromosome 5. IX. Sequence features of the regions of 1,011,550 bp covered by seventeen
                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato T., Shimizu T., Watarai M., Kobayashi M., Kano S., Hamabata T., Yamasaski S., Takeda Y., Yamasaski S., Takeda Y., "Genomic sequence of Shiga toxin 2-converting phage isolated from Escherichia coli 0157:H7 Okayama strain and comparison with other Shiga toxin 2-converting phages."; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AP004402; BAB87947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Peprantophyta, Peprantophyta, Magnoliophyta, Lillopsida, Asparagales, Hemerocallidaceae, Hemerocallis.
VCBI_TaxID=80862;
                                                                                                                                                                                  0;
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                                                                                                                                                     58.2%; Score 39; DB 10; Length 866; 50.0%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               56.7%; Score 38; DB 9; Length 108; 60.0%; Pred. No. 7.5; ttive 1; Mismatches 3; Indels
                                                                                                                                                                                5; Indels
                                                                               Pland TAC clones.";
DNA Res. 6:183-195(1999),
EMBL, ABO18113, BAB09775.1;
SEQUENCE 866 AA; 100187 MW; 164FAB99B4976D27D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 108 AA; 12279 MW; 2FF2E76690C78BA7 CRC64;
                                                                                                                                                                                                                                                                                                                                 01-UNN-2002 (TrEMBLrel. 21, Created)
01-UNN-2002 (TrEMBLrel. 21, Last sequence update)
01-UNN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 12.3 kDa protein.
Stx2 converting bacteriophage I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998 (TrEMBLrel. 08, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Senescence-associated protein 3 (Fragment).
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               MEDLINE=99397451; PubMed=10470850;
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Best Local Similarity
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STRAIN=CV. COLUMBIA;
STRAIN=CV. COLUMBIA;
Lin X., Faul S., PubMed=10617197;
Lin X., Kaul S., Rounaley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo, H., Moffat K.S.,
Cronin L.A., Shen M., VanAken S.B., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, euroside II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lin X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007170; AAD25641.1; -
InterPro; IPR004264; Transposase_23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF03017; Transposase 23; 1. SEQUENCE 531 AA; 60512 WW; 57B3AC60C976A4B9 CRC64;
                                                           (TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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077855;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
PRT;
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En/Spm-like transposon protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 402:761-768(1999).
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MEDLINE=95191002; PubMed=7884875;
Mulder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J.,
Scherphier H.J., de Perre P., Boer K., Goudsmit J.;
Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is unrelated to time of HIV-1 RNA positivity in the child.";
J. Virol. 69:2285-2296(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=95191002; PubMed=7884875; Milder-Kampinga G.A., Simonon A., Kuiken C.L., Dekker J., Scherpbier H.J., de Perre P., Boer K., Goudsmit J., Scherpbier H.J., de Perre P., Boer K., Goudsmit J., "Similarity in env and gag genes between genomic RNAs of human immunodeficiency virus type 1 (HIV-1) from mother and infant is unrelated to time of HIV-1 RNA positivity in the child."; J. Virol. 69:2285-296(1995).

EMBL: 247868; CAR87882.1; -.

EMBL: 247868; CAR87882.1; -.

FinterPro; IPRO0777; GP120.

Pfam; PRO0516; GP120.

Pfam; PRO0516; GP120.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 55.2%; Score 37; DB 15; Length 91; Best Local Similarity 60.0%; Pred. No. 9.9; Matches 6; Conservative 2; Mismatches 2; Indels
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91 AA; 10530 MW; 8B10C62011F305D6 CRC64;
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                                                                 Human immunodeficiency virus type 1.
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Envelope protein (Fragment).
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Viruses; Retroid viruses; Retroviridae; Lentivirus.
VCBI_TaxID=11676;
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BMEN; Z47865', CA8A61881.1;
InterPro; IPRO00777; G9120.
Pfam; PF00516; GP120; 1.
AIDS; Coat protein; Glycoprotein.
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Search completed: February 21, 2003, 08:00:42 Job time : 21.6744 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

February 21, 2003, 07:37:21 ; Search time 28.093 Seconds Run on:

(without alignments) 56.918 Million cell updates/sec

US-09-743-107B-88

1 CFQWXRNMRKVR 12 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_101002:*

| SIDSZ/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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| SIDSZ/gcgdata/geneseqg-embl/AA1989.DAT:*
| SIDSZ/gcgdata/geneseqg-embl/AA1989.DAT:* | SIDS2/gcgdata/geneseq_genese

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Human lactoferrin									
SUMMARIES			ID		AAY78038	AAY78046	AAY78047	•		AAY78088	AAY78091	AAY78092	AAY78037
			DB	21	21	21	21	21	21	21	21	21	21
			Match Length DB 1	12	12	12	12	12	12	12	12	12	13
	₩	Query	Match	98.5	97.0	97.0	97.0	97.0	97.0	97.0	97.0	97.0	97.0
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ALIGNMENTS

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AAY78072 standard; Peptide; 12 AA.
              25-APR-2000 (first entry)
         AAY78072;
RESULT 1
  AAY78072
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Human lactoferrin derived peptide SEQ ID NO:72.

Human; lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.

Homo sapiens. Synthetic.

WO200001730-A1. 13-JAN-2000.

99WO-SE01230 06-JUL-1999; 06-JUL-1998;

98SE-0002441. 98SE-0002562. 98SE-0004614. 17-JUL-1998; 29-DEC-1998;

Hanson LA, Mattsby-Baltzer I, Baltzer L, (ASCI-) A+ SCI INVEST AB.

Dolphin GT;

WPI; 2000-147388/13.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives.
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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                  New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                    Claim 22; Page 35; 102pp; English
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              binding to specific lattoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, collis, and Candida infection on a mucosal membrane), inflammations and/or tummours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and the contact of the costs. Therefore is the same purposes as lactoferrin at lower and a contact of the costs.
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fungicidal and bactericidal and may also be used as preservatives.
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Pred. No. 4.7e-05;
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98SE-0002562.
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Best Local Similarity
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                                              Length 12;
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                                              Score 65; DB 21;
Pred. No. 4.7e-05;
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AAY78088 standard; Peptide; 12 AA.

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through chiding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as and and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                                                                                                                                                                                                      food, infant formula, anti-inflammatory, anti-microbial, anti-tumour, urinary tract infection; colitis, Candida infection; fungicidal; bactericidal; preservative.
                                                                                                                                                                                                                                                                                     Human; lactoferrin; modification; infection; inflammation; tumour;
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                                                                                                                                                                                                                                                 Human lactoferrin derived peptide SEQ ID NO:87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baltzer L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 22; Page 37; 102pp; English.
                                                                                                                                  AAY78087 standard; Peptide; 12 AA
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98SE-0002562.
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CFOWXRNMRKVR 12
                                  1 CFOWERNMRKVR 12
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                                                                                                                                                                       AAY78087;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
                                                                                                                 Human, lactoferrin, modification; infection; inflammation; tumour; food; infant formula, anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal; bactericidal; preservative.
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100.0%; Pred. No. 4.7e-05;
ive 0; Mismatches 0; Indels
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                                                                                        Human lactoferrin derived peptide SEQ ID NO:88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 22; Page 37; 102pp; English:
                                                                                                                                                                                                                                                                                                                                        98SE-0002441.
98SE-0002562.
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                                                           (first entry)
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Best Local Similarity 100.
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                             AAY78088;
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Human lactoferrin derived peptide SEQ ID NO:91.

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Gaps

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Best Local Similarity 100. Matches 12; Conservative

Matches

RESULT 7

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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also tungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower and anti-tumoural actoferrin at lower and actofer and actofer and actofer and anti-tumoural actofer and actofer an
                     Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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98SE-0004614.
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                                                                                                                                                                               sapiens
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                                                                                                                                                                                                        Synthetic.
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AAY78001 to AAY78100 represent peptides having sequences based on human binding to specific lactoferrin receptors and are through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candida infections a merosal membrane), inflammations and/or tumours. The peptides can also be used fungicidal and have formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Byen though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they

New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food

Claim 22; Page 38; 102pp; English.

Dolphin GT;

Baltzer L,

Mattsby-Baltzer I,

Hanson LA,

WPI; 2000-147388/13

(ASCI-) A+ SCI INVEST AB.

17-JUL-1998; 29-DEC-1998;

99WO-SE01230. 98SE-0002441. 98SE-0002562. 98SE-0004614.

06-JUL-1999; 06-JUL-1998;

WO200001730-A1

Synthetic.

13-JAN-2000

cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower

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Human, lactoferrin; modification; infection; inflammation; tumour; food; infant formula; anti-inflammatory; anti-microbial; anti-tumour; urinary tract infection; colitis; Candida infection; fungicidal;
                                                                                                                                                        Human lactoferrin derived peptide SEQ ID NO:37.
                                                                                 AAY78037 standard; Peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                             99WO-SE01230.
                                                                                                                                                                                                                   bactericidal; preservative
                                                                                                                               25-APR-2000 (first entry)
1 CFOWXRNMRKVR 12
                       1 CFOWKRNMRKVR 12
                                                                                                                                                                                                                                                                             WO200001730-A1.
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Gaps

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97.0%; Score 65; DB 21; Length 12; larity 91.7%; Pred. No. 4.7e-05; Conservative 0; Mismatches 1; Indels

Local Similarity nes 11; Conserv

12 AA;

Sequence

Query Match Best Local 9 Matches 13

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Score 65; DB 21; Lengtn 12;
Pred, No. 4.7e-05;
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                                                                 0; Mismatches
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                                                                 11; Conservative
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AAY78092

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Homo sapiens

Dolphin GT;

Baltzer L,

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Mattsby-Baltzer I,
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                    WPI; 2000-147388/13
                                                                                                                                                                                                                                                                                                      Local Similarity
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29-DEC-1998;
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 Hanson LA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as uninary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; lactoferrin; modification; infection; inflammation; tumour;
food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                  New peptides used for treatment and prevention of infections,
                                                                                                                             inflammations and tumors and for use in infant formula food
                                                                                                                                                                                                                                                                                                                                                                    97.0%; Score 65; DB 21; Length 13;
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                                                                          Dolphin GT
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0; Mismatches
                                                                         Mattsby-Baltzer I, Baltzer L,
                                                                                                                                                 Claim 12; Page 70; 102pp; English.
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98SE-0002562.
98SE-0004614.
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                    98SE-0002562
98SE-0004614
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                                                    (ASCI-) A+ SCI INVEST AB.
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                                                                                                                                                                                                                                                                                                                                                                                                             1 CFQWXRNMRKVR 12
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                                                                                             WPI; 2000-147388/13
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                    17-JUL-1998;
29-DEC-1998;
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                                                                          Hanson LA,
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AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
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New peptides used for treatment and prevention of infections, inflammations and tumors and for use in infant formula food
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                                                                                                                                 Claim 15; Page 74; 102pp; English.
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98SE-0002562.
98SE-0004614.
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                           AAY78001 to AAY78100 represent peptides having sequences based on human lactoferrin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the direction. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and candia infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula food. The peptides are also in food stuffs such as infant formula also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin at lower enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative
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                                                                                                                                                                                                                                                                                                                                  Score 65; DB 21; Length 13;
Pred. No. 5e-05;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY78036 standard; Peptide; 14 AA.
Claim 18; Page 74; 102pp; English.
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91.7%;
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                                                                                                                                                                                                                                                                                                  13 AA;
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29-DEC-1998;
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AAY78036
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urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used in food stuffs such as infant formula food. The peptides are also fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                                                                                                                                                                             Score 65; DB 21; Length 14;
Pred. No. 5.4e-05;
0; Mismatches 1; Indels
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98SE-0002562.
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Best Local Similarity 91...,
Best 11; Conservative
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29-DEC-1998;
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lactoferin. The peptides are taken up in the intestine through binding to specific lactoferrin receptors and are then transported through the circulation. A medicinal product of the peptide or fragment can be used for treating and/or prevention of infections (such as urinary tract infections, colitis, and Candida infection on a mucosal membrane), inflammations and/or tumours. The peptides can also be used fund scutts such as infant formula food. The peptides can also be used fungicidal and bactericidal and may also be used as preservatives. Even though native human lactoferrin have been shown to have desired anti-inflammatory anti-infectious and anti-tumoural properties they cannot be used clinically on a broad basis because of high production costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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food; infant formula; anti-inflammatory; anti-microbial; anti-tumour;
urinary tract infection; colitis; Candida infection; fungicidal;
bactericidal; preservative.
costs. Therefore, provision of peptides based on lactoferrin would enable them to be used for the same purposes as lactoferrin at lower
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                                                                                                    97.0%; Score 65; DB 21; Length 14; 91.7%; Pred. No. 5.4e-05; ive 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 18; Page 75; 102pp; English.
                                                                                                                                                                                                                                                                                                     AAY78051 standard; Peptide; 14 AA.
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98SE-0002562.
98SE-0004614.
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                                                                                                                                          11; Conservative
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                                                                                                                         Best Local Similarity
                                                                     14 AA;
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17-JUL-1998;
29-DEC-1998;
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97.0%; Score 65; DB 21; Length 14;

Query Match

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91.7%; Pred. No. 5.4e-05;
tive 0; Mismatches 1;
                                                                                                                                                  Search completed: February 21, 2003, 07:56:43 Job time : 29.093 secs
                     11; Conservative
                                                        1 CFOWXRNMRKVR 12
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Best Local Similarity
Matches 11; Conserv
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us-09-743-107b-88.rai

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FEATURE:
NAME/KEY: Peptide
LOCATION: 1..18
OTHER INFORMATION: /note= "HUMAN LACTOFERRIN PEPTIDE
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MOLECULE TYPE: peptide
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STRANDEDNESS: single
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                                                                                                             February 21, 2003, 07:50:40; Search time 8.93023 Seconds (without alignments) 39.537 Million cell updates/sec
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Sequence 6
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-07-87-91-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-91-93-
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US-08-464-182A-5
US-08-406-271-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3-08-485-948-8
3-08-628-380-8
3-08-475-055-8
                                                                                                                                                                                                                                                                                                                                      262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                        BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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67
                                                                                                                                                                                                                                   1 CFQWXRNMRKVR 12
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Match Length DB
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                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
                                                                                                                 Run on:
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Sequence 2, Apr Sequence 2, Apr Sequence 2, Apr Sequence 2, Apr Sequence 2, Apr Sequence 4, App Sequence 4, App Sequence 4, App Sequence 4, App Sequence 2, App		2
54 2 US-08-464-182A-2 54 2 US-08-466-271-2 694 3 US-08-744-586-2 694 4 US-09-421-632-2 694 4 US-09-932-190-2 705 2 US-08-655-640-4 711 1 US-08-155-640-4 711 3 US-08-165-640-4 711 3 US-08-165-640-4 711 1 US-08-165-640-4 711 1 US-08-165-67-4 711 1 US-08-168-17-1 711 1 US-08-165-108-2 711 2 US-08-456-108-2 711 3 US-08-456-108-2 711 3 US-08-456-108-2 711 3 US-08-456-108-2 711 4 US-08-456-108-2 711 4 US-08-456-108-2	ALIGNMENTS	Judica 18 - 204 - 487 - 3 Judica 23 Application US/08204487 Judica 24 - 487 - 3 APPLICANT: NAMARAINA, HIDEKI APPLICANT: NAMARAINA, HIDEKI APPLICANT: NOSUCHI, WATARU APPLICANT: TANAKA, SHIGEAKI ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBEAULT STREET: SA STATE STREET CITY: BOSJON STATE: MA COMPUTER: LEM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PACHILIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICANTON NUMBER: US/08/204,487 TELEPRINE CANARATION: NAME: CAMPBELL, PAULA A. REGISTRATION NUMBER: 32,503 REGISTRATION NUMBER: 32,503 REGISTRATION NUMBER: 32,503 REFERENCE POCKET NUMBER: 32,503 REFERENCE POCKET NUMBER: 32,503 REFERENCE POCKET NUMBER: 32,503 TELEPRINE: (617) 248-7100 TELEBRINE: (617) 248-7100
9977.00 9977.00 9977.00 9977.00 9977.00 9977.00		19. Application 19. Application 10. S565425 2DANT: YAMAMOTO CANT: NAKASHIM CANT: NAKASHIM CANT: TANAKA, CANTION: CANTION: CANTION: CANTION: CANTING SYSTEM: CAMPBELL, PA: CANTING SYSTEM: CAMPBELL, PA: CANTING SYSTEM: CAMPBELL, PA: CAMBELL, PA: CAMBBELL,
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		SEQUENCE 3, APPLICATION US/C SEQUENCE 3, APPLICATION SEGSASS GENERAL INFORMATION: APPLICANT: YAMAMOTO, NAC APPLICANT: NAKASHIMA, HI APPLICANT: NAKASHIMA, HI APPLICANT: NAKASHIMA, HI APPLICANT: NAKASHIMA, HI APPLICANT: TANAKA, SHIGE APPLICANT: OCHIDA, TOSHI TITLE OF INVENTION: INHI NUMBER OF SEQUENCES: 8 CORRESPONDENCE SE ADDRESSE: THIBEAULT STREET: 3 STATE STREE CITY: SOSTON STREET: 3 STATE STREE CUTY: NOA COUNTY: USA ZIP: NA COMPUTER: IBM PC COMPA OPPLICATION SYSTEM: PC-D-D SOFTWARE: PATENT PO-D SOFTWARE: PATENT PRO- SOFTWARE: PATENT NO NUMBER: US FILING DATE: 02-MAR-19 CLASSIFICATION NUMBER: US RESERENCE/DOCKET NUMBER: REGISTRATION NUMBER: S REFERENCE/DOCKET NUMBER TELEPHONE: (GIT) 248-71 TELEPHONE: (GIT) 248-71 TELEPHONE: (GIT) 248-71 TELEPHONE: GIT) 248-71
8 9 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		RESULT 1 US-08-204-487 Sequence 3, Patent No. GENERAL IN APPLICAN CORPUTER COMPUTER COMPUTER APPLICA COMPUTER APPLICA APPLICA COMPUTER APPLICA APPLIC

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COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 Hackensack Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNATION TO STATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amittering.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 411 nac.
CITY: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFQWXRNMRKVR 12
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                                                                                                   US-08-628-380-8
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US-08-475-055-8
                                                                     RESULT 3
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                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                         RESULT 2
US-08-485-948-8
US-08-485-948-8

i Sequence 8, Application US/08485948

i Patent No. 5855882

i GENERAL INFORMATION:

APPLICANT: YOUG MING LI
APPLICANT: HELEN VLASSARA

APPLICANT: HELEN VLASSARA

TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION

TITLE OF INVENTION: ENDPRODUCTS, AND METHODS OF THEIR USE
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                                                                                                Length 18;
                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,948
                                                                                         Score 65; DB 1; I
Pred. No. 3.6e-05;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26,742
ER: 947-1-008A
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
FILING DATE: APRLL 7, 1995
CLASSIFUCATION NUMBER: 08/418,642
FILING DATE: APRLL 7, 1995
GLASSIFUCATION: 436
ATTORNEY/AGENT INFORMATION:
RAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
FERERENCE/DOCKET NUMBER: 947-1-06
TELEPHONE: 201 487-5800
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SECTEMES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
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INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 18 amino acids TYPE: amino acids
OTHER INFORMATION: (20-37)"
                                                                                         97.0%;
91.7%;
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DESCRIPTION: LF-C1, 8-25
                                                                                         Query Match
Best Local Similarity 91.7
Matches 11; Conservative
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                                                                                                                                                                                                                    1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                   1 CFOWORNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Jersey
: USA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
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US-08-204-487-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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Sequence 8, Application US/08628380
Patent No. 5891341
GENERAL INFORMATION:
APPLICANT: LI, YONG MING
APPLICANT: VLASSARA, HELEN
APPLICANT: CAPAMI, ANTHONY
TILLE OF THE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application US/08475055;
Patent No. 5562245
GENERAL INFORMATION:
APPLICANT: YOUR MING LI
APPLICANT: ANTHONY CERAMI
TITLE OF INVENTION: AGENTS FOR BINDING TO ADVANCED GLYCOSYLATION
TITLE OF INVENTION: BUDPRODUCTS, AND METHODS OF THEIR USE
NUMBER OF SEQUENCES: 9
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SOFTWARE PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/628,380
FILING DATE: April 4, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION S14
ATTONNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REGISTRATION INFORMATION:
TELEPRAK: 201 487-580
TELEPRAK: 201 487-580
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97.0%; Score 65;
            OPERATING SYSTEM: MS-DOS
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NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION IN GENOME:
CHROMOSOME/SEGMENT
MAP POSITION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
HYPOTHETICAL:
ANTI-SENSE:
FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM:
STRAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-755-161A-3
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Pred. No. 3.6e-05;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3, Application US/07755161A
Fatent No. 5304633
GENERAL INFORMATION:
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Xb
                                                                                                                      COMPUTER CASABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,055
FILNG DATE:
CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/485,948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 947-1-008A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
                                                                                                                                                                                                                                                                                                                                         FILING DATE:
APPLICATION NUMBER: 08/488,217
FILING DATE: JUNE 7, 1995
APPLICATION NUMBER: 08/418,642
FILING DATE: APRIL 7, 1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97.08;
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX: 133521
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
DESCRIPTION: LF-C1, 8-25
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 18 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: NO
; FRAGMENT TYPE: internal
US-08-475-055-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
                                                                          STATE: New Jersey COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWORNMRKVR 12
                                                                                                              07601
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US-07-755-161A-3
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LOCATION: 19
IDENTIFICATION METHOD:
OTHER INFORMATION: /note=""thiol group of
OTHER INFORMATION: Cys residue at location 19 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: modified site
LOCATION: 2
LOCATION: 2
LOCATION: 7
LOCATION:
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
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Length 20;

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LOCATION: 19

IDBNIFTCATION METHOD:
OTHER INFORMATION: ()note= "thiol group of OTHER INFORMATION: ()s residue at location 19 connected by disulfide bond with OTHER INFORMATION: ()s residue at location 19 connected by Alsulfide bond with PUBLICATION INFORMATION: () AND Group of Cys residue at location 2" AUTHORS:
AUTHORS:
        LOCATION: 2
IDBNIFTATION METHOD:
OTHER INFORMATION: (Anote= "thiol group of OTHER INFORMATION: Cys residue at location 2 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 19"
FEATURE:
NAME/KEY: modified site
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APPLICANT: NAKASHIMA, HIDEKI
APPLICANT: MAKASHIMA, HIDEKI
APPLICANT: MOSUCHI, WATARU
APPLICANT: TONAKA, SHIGBAKI
APPLICANT: TOSAKO, SHINY ICHI
APPLICANT: WAMASAKI, YOSHIMIRO
APPLICANT: UCHIDA, TOSHIMKI
TITLE OF INVENTION: VIRAL INFECTION AND PROLIFERATION
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 65; DB 1; Length 20; Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ & ADDRESSEE: THIBBAULT STREET: 53 STATE STREET CITY: BOSTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204,487
FILING DATE: 02-WAR-1994
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FJN-019
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 1, Application US/08204487; Patent No. 5565425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, PAULA A.
REGISTRATION NUMBER: 32,53
REFERENCE/DOCKET NUMBER: FJN-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                           DOCUMENT NUMBER:
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VOLUME:
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US-08-204-487-1
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                            ö
Best Local Similarity 91.7%; Pred. No. 4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500KD
COMPUTER: Diskette, 5.25 inch, 500KD
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: DisplayWrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-SEP-1991
ATMINEY/AGENT INFORMATION:
ATMINEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REPRENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: modified site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
                                                              1 CFOWXRNMRKVR 12
                                                                                                     2 CFÓWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
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IMMEDIATE SOURCE:
LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAPLOTYPE:
TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: D.C
COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CELL TYPE:
CELL LINE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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us-09-743-107b-88.rai

US-08-256-771-24

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GENERAL INFORMATION:

APPLICANT: Mamoru TOMITA et al.

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING
TITLE OF INVENTION: PRODUCTS THEREWITH
NUMBER OF SEQUENCES: 32
CORRESPONDENCE Menderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                        .;
0
                                                                                                                                                                                                                                                                                                                          Score 65; DB 1; Length 20;
Pred. No. 4e-05;
                                                                                                                                                                                                                                                                                                                                                                      1; Indels
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OTHER INFORMATION: /note= "Cys residues are linked by
OTHER INFORMATION: disulfide bond"
                                                                                                                                                                                                                                       /note= "ANTIBACTERIAL PEPTIDE
DERIVED FROM HUMAN LACTOFERRIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible COMPUTER: IBM Compatible COMPUTER: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
CLASSIPICATION: 514
PRIOR APPLICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 24, Application US/08256771
Patent No. 5656591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24:
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 aming acids
                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 91.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                   TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                      NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                       1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20005
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US-08-256-771-24
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                                             Gaps
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Patent No. 5655591

GENERAL INFORMATION:

TITLE OF INVENTION: ANTIMICROBIAL AGENTS AND METHOD FOR TREATING

TITLE OF INVENTION: PRODUCTS THEREWITH

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

STREET: 0.C.

STREET: 0.C.

STREET: 0.C.

STREET: 0.C.
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                                               0;
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0
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; OTHER INFORMATION: /note= "Cys residues are protected to 'THER INFORMATION: prevent disulfide bond"
US-08-256-771-25
97.0%; Score 65; DB 1; Length 20; 91.7%; Pred. No. 4e-05; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
97.04; Score 65; DB 1; Length 20;
Best Local Similarity 91.74; Pred. No. 4e-05;
Matches 11; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 kb COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,771
FILING DATE: July 22, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TRNGTH: 20 amino acids
                                         11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514 PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                              1 CFQWXRNMRKVR 12
                                                                                                            2 CFQWQRNMRKVR 13
                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 CFOWORNMRKVR 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
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                                                                                                                                                                                               US-08-256-771-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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    Query Match
                                       Matches
                                                                                                                                                                              RESULT 9
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RESULT 10 US-08-381-984-24

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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "the specified peptide as well as
OTHER INFORMATION: peptides including the specified peptide as a fragment there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Samyang Genex Corporation
TITLE OF INVENTION: Mass production method of lactoferrin polypeptide from yeast and
TITLE OF INVENTION: useful microorganism thereof
FILE REPERBYCE: PA/SYG/00139
CURRENT APPLICATION NUMBER: US/09/508,734
CURRENT FILING DATE: 2000-06-01
PRIOR APPLICATION NUMBER: PCT/RK99/00373
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1999-07-14
PRIOR PILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Kopatentin 1.71
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are chemically modified to prevent disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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             805 Fifteenth Street, N.W., #700
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
                                                                                                                                                             COMPUTER: IBM Compatible
OPREATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION UDMIR:
APPLICATION NUMBER: US/08/381,984
FILING DATE: April 11, 1995
CLASSIFICATION: 252
PRIOR APPLICATION: 252
PRIOR APPLICATION: APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-508-734-4; Sequence 4, Application US/09508734; Patent No. 6423509; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367 REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850 TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CFOWORNMRKVR 13
                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                           D.C.
: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                  20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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                                                                               COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-381-984-25
               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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Matches
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; OTHER INFORMATION: /note= "the specified peptide as well as

OTHER INFORMATION: peptides including the specified peptide as a fragment thereo

US-08-381-984-24
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IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "cysteine residues at positions 2
OTHER INFORMATION: and 19 are bonded by disulfide linkage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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Pred. No. 4e-05;
0; Mismatches 1; Indels
Sequence 24, Application US/08381984
Fatent No. 5804555
GENERAL INFORMATION:
APPLICANT: Mamoru TOMITA et al.
ITILE OF INVENTION: ANTIOXIDANT
NUMBER OF SEQUENCES: 32
COMBERSPONDENCE ADDRESS:
ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb COMPUTER: IDM Compatible COMPUTER: IDM COMPATIBLE SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/381,984 FILING DATE: April 11, 1995.
CLASSIFICATION: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25, Application US/08381984
Fatent No. 5804555
GENERAL INFORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ANDESS:
ADDRESSEE: Wenderoth, Lind & Ponack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ch 97.0%;
1 Similarity 91.7%;
11; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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                                                                                                                                                                             STREET: 805 Fifte
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                        D.C.
(: U.S.A.
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Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                  20002
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                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION:
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LOCATION: 21
IDENTIFICATION METHOD:
IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4"
AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IDENTIFICATION METHOD:
OTHER INFORMATION: /note= "thiol group of
OTHER INFORMATION: Cys residue at location 4 connected by disulfide bond with
OTHER INFORMATION: thiol group of Cys residue at location 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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             FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-07-755-161A-10
                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: AMINO ACID STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified site LOCATION: 21
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                                                                                                                                                                  TELEFAX: 202-371-8856
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                              linear
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CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
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                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAP POSITION:
UNITS:
                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                           ANTI-SENSE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

Sequence 6, Application US/09508734

Sequence 7. Application US/09508734

GENERAL INCORMATION: useful microarganism thereof

TITLE OF INVENTION: useful microarganism thereof

FILE REFERENCE: PA/SYG/00139

CURRENT APPLICATION NUMBER: US/09/508,734

CURRENT APPLICATION NUMBER: PCT/KR99/00373

PRIOR APPLICATION NUMBER: RC199-07-14

PRIOR APPLICATION NUMBER: RR1998-29351

FRIOR APPLICATION DATE: 1999-07-13

SOFTWARE TLING DATE: 1998-07-13

NUMBER OF SEQ ID NOS: 12

SOFTWARE: KOPALENTIN 1.71
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                                                                                                                                                                0;
                                                                                                            97.0%; Score 65; DB 4; Length 22; 91.7%; Pred. No. 4.4e-05; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                97.0%; Score 65; DB 4; Length 24; 91.7%; Pred. No. 4.8e-05; 1: Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Application US/07755161A
Patent No. 5304633
GENERAL INPORMATION:
APPLICANT: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS: ADDRESSE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/755,161A
FILING DATE: 19910905
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                          Query Match
Best Local Similarity 91.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 97.0
Best Local Similarity 91.7
Matches 11; Conservative
                    TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
CORGANISM: Homo sapiens
US-09-508-734-6
                                                                                                                                                                                                1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                        2 CFÓWQRNMRKVR 13
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STATE: D.C.
COUNTRY: U.S.A.
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                                               ; ORGANISM: HI
US-09-508-734-4
LENGTH: 22
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Search completed: February 21, 2003, 08:04:25 Job time: 8.93023 secs
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Best Local Similarity
Matches 11; Conservat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 CFOWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CFOWORNMRKVR 15
                                                                                                                                                                                                                                                       DOCUMENT NUMBER:
                                                                                                                                                                                                                                                                                                                                           US-07-891-174-10
                                                                                                                             TITLE:
JOURNAL:
VOLUME:
                                                                                                                                                                                            ISSUE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DP.
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                                   Sequence 10, Application US/07891174
Patent No. 5317084
GENERAL INFORMATION:
APPLICART: Mamoru TOMITA et al.
TITLE OF INVENTION: Antimicrobial Peptides and an TITLE OF INVENTION: Antimicrobial Agent
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
                                                                                                                                                                                                                                                              STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/755,161
FILING DATE: 05-58P-1991
ATTOMEN'AGENT INFORMATION:
NAME: Warren M. Cheek Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION INFORMATION:
TELECHMUNICATION 18950
TELEFAX: 202-371-8850
                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: DisplayWite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/891,174
FILING DATE: 29-MAY-1992
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 amino acids TYPE: amino acid STRANNEDNESS: single STRANNEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAP POSITION:
UNITS:
FEATURE:
NAME/KEX: modified site
LOCATION: 4
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: modified site LOCATION: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE TYPE:
CELL TYPE:
CELL LINE:
CRLL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1i)
MOLECULE TYPE:
HYPOTHETICAL:
RESULT 15
US-07-891-174-10
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OTHER INFORMATION: /note= "thiol group of OTHER INFORMATION: Cys residue at location 21 connected by disulfide bond with OTHER INFORMATION: thiol group of Cys residue at location 4" AUTHORS AUTHORS.
                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 .
0
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PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
IDENTIFICATION METHOD:
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(without alignments)
54.162 Million cell updates/sec
                                                                                                                                                                      February 21, 2003, 08:08:15; Search time 6.88372 Seconds
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| Cgn2_6/ptodata/2/pubpaa/DCT_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US06_PUBCONB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
| Cgn2_6/ptodata/2/pubpaa/US08_PUBCONB.pep:*
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156504 Begs, 31069816 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Published_Applications_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                               US-09-743-107B-88
67
                                                                                                                                                                                                                                                                                                                                                          1 CFQWXRNMRKVR 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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                                                                                                                                                                                                                                                                                                                                                          Seguence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                          Run on:
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11: /cgn2_6/ptodata/2/pubpa/0310_NEW PUB.pep:* 12: /cgn2_6/ptodata/2/pubpa/0310_NEW PUB.pep:* 13: /cgn2_6/ptodata/2/pubpa/US10_PUBCOMB.pep:* 14: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:* 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* 16: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* 16: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* 17: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*	a/usug Fubcoms.pep:* a/usio_nbw Fub.pep:* a/usio_nbw Fub.pep:* a/useo_nbw Pub.pep:* a/useo_nbw Pub.pep:*
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er e	Description		sequence z, Appli	Segmence zu, Appi		Semience 3, Appli	, ה ה			٠,	Semionde 2 April :	Semionice 2, Appli	Semiono 20 Appli	4 -	Semience 30, Appr	Segment 17905, A	Somice 3/13, Ap		113,	
SUMMARIES	ID	IIS-09-798-869-2	11S-09-798-865-20	US-10-023-096-2	9-698-862-60-SN	US-09-798-869-3	US-09-798-869-23	US-09-798-869-7	US-09-798-869-4	US-09-798-869-22	US-09-888-320-2	US-09-798-86-8	US-09-798-869-20	US-09-798-868-30		-		TISTURE 070 - 011 0	ETT-WC67-016 C0 00	0
	Query Match Length DB	15 9	25	694 9	15 9	15 9	25 9	15 9	15 9	25 9	489 9	15 9	15 9	15 9	21 10	96	95 10	338 9	0 1	סמננ
عبن	Query Match	97.0	97.0	97.0	85.1	71.6	71.6	59.7	58.2	58.2	55.2	53.7	53.7	53.7	52.2	50.7	50.7	50.7		-
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	Result No.	1	7	m	4	5	9	7	8	σ	10	11	12	13	14	15	16	17	0	٥

Sequence 119, App Sequence 14, Appl Sequence 14, Appl Sequence 24, Appl Sequence 30, Appl Sequence 2, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 3, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 5, Appl Sequence 6, Appl Sequence 6, Appl Sequence 6, Appl Sequence 12129, Appl Sequence 12129, Appl Sequence 12129, Appl Sequence 12129, Appl Sequence 107, App Sequence 26, Appl Sequence 107, App Sequence 26, Appl Sequence 107, App Sequence 26, Appl Sequence 3, Appl Sequence 3, Appl Sequence 26, Appl Sequence 3, Appl Seque	Sequence 13, Appl Sequence 33, Appl
9 US-09-999-832A-119 9 US-09-978-189-119 10 US-09-978-189-119 10 US-09-981-649A-24 11 US-09-981-649A-24 12 US-09-981-649A-30 13 US-09-981-649A-32 14 US-09-981-649A-32 15 US-09-981-649A-32 16 US-09-981-649A-32 17 US-09-981-649A-3 18 US-05-192-48-3 18 US-10-219-24B-3 19 US-10-219-24B-5 10 US-09-865-722-5 10 US-09-865-722-5 10 US-09-864-761-46393 10 US-09-864-761-46393 10 US-09-864-761-46393 10 US-09-864-761-46393 10 US-09-861-723-26 10 US-09-861-723-26 10 US-09-861-723-26 10 US-09-861-723-26 10 US-09-861-723-26 10 US-09-861-723-26 10 US-09-861-732-6 10 US-09-861-822-107 10 US-09-861-822-107 10 US-09-861-822-107 10 US-09-861-822-107	US-09-956-206A-13 US-09-735-056-33
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97.0%; Score 65; DB 9; L
Best Local Similarity 91.7%; Pred, No. 1.8e-05;
Matches 11; Conservative 0; Mismatches 1:
               Sequence 2, Application US/09798869
Publication No. US20030022621A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: APPLICANT: APPLICANT: BALDUR SVEINBU (RNSSON
APPLICANT: LARS VORLAND
ITTLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FREEEEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
APPLICANT: (YSTEIN REKOAL
APPLICANT: HALDUR SVEINBJ (RNSSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-798-869-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CFQWXRNMRKVR 12
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US-09-798-869-2
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RESULT 5
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APPLICANT: Kruzel, Marian L.
APPLICANT: Kruzel, Tomasz
APPLICANT: Gollnick, Paul D.
APPLICANT: Gollnick, Paul D.
APPLICANT: Doyle, Darrell J.
TITLE OF INVENTION: Cloning, Expression, and Uses of Human
                                                                                                                                                                                                                                                                                                                                                                                      97.0%; Score 65; DB 9; Length 25; 91.7%; Pred. No. 2.9e-05; 1ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Jacobson, Price, Holman & Stern STREET: 400 Seventh St. N.W.
CITY: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20004
COMPUTER READABLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,096
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILLING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PRASISEQ for Windows Version 4.0
SSOTUMARE: PASISEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10505/P58185C
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APPLICATION NUMBER: US/08/724,586
FILING DATE: 30-SEPT-1996
APPLICATION NUMBER: US 08/238,445
FILING DATE: 05-MAX-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/10023096
; Patent No. US20020160941A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Player, William E. REGISTRATION NUMBER: 31,409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 10:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 393-5950
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 694 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                      11; Conservative
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MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo Sapiens
US-09-798-869-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CFQWXRNMRKVR 12
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Best Local Similarity
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US-10-023-096-2
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                                                               0
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0
Query Match 97.0%; Score 65; DB 9; Length 694; Best Local Similarity 91.7%; Pred. No. 0.00066; Matches 11; Conservative 0; Mismatches 1; Indels
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Pred. No. 0.00044;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                               SQUENCE 6, Application US/09798869
| Publication No. US20030022821A1
| GENERAL INFORMATION:
| APPLICANT: COHN SIGURD SVENDSEN
| APPLICANT: CYSTEIN REKDAL
| APPLICANT: HALDWS SVETINBJ (RNSSON
| APPLICANT: LARS VORLAND
| TITLE OF INVENTION: BIOACTIVE PEPTIDES
| TITLE OF INVENTION: BIOACTIVE PEPTIDES
| FILE REFERENCE: A44049-PCT-USA-A
| CURRENT APPLICATION NUMBER: PCT/GB99/02851
| PRIOR APPLICATION NUMBER: PCT/GB99/02851
| PRIOR APPLICATION NUMBER: GB9818938.4
| PRIOR FILING DATE: 1998-08-31
| PRIOR FILING DATE: 1998-08-38
| NUMBER OF SEQ ID NOS: 30
| SEQ ID NO S: SEQ ID NOS: 30
| LIBNGTH: 15
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Publication No. US20030022821A1
GENERAL INPORMATION:
APPLICANT: (YSTEIN REXDAL
APPLICANT: (YSTEIN REXDAL
APPLICANT: BALDUR SVEINBU (RNSSON
APPLICANT: AA4049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT RILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: PCT/GB99/02851
PRIOR APPLICATION NUMBER: GB9818938.4
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FARLSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 85.1%;
Best Local Similarity 93.3%;
Matches 10; Conservative
                                                                                                        1 CFQWXRNMRKVR 12
                                                                                                                                                            22 CFÓWORNMRKVR 33
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Best Local Similarity
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                                                                                                                                                                                                                                      RESULT 4
US-09-798-869-6
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2; Mismatches

7; Conservative

Matches

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58.2%; Score 39; DB 9; Length 25; 54.5%; Pred. No. 0.97; 1. Mismatches 4; Indels
                                                                                                                                                                                                             APPLICANT: JOHN SIGNED SVENDSEN
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
ITILE OF INVENTION: BIOACTIVE PEPTIDES
FILE REPRENENT: AJ404-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR PILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-13
PRIOR FILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FABLESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: (YSTEIN REKDAL
APPLICANT: BALDUR SYBINBJ (RNSSON
TITLE OF INVENTION: BIODREST (RNSSON
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: CT/GB99/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                        ; Sequence 4, Application US/09798869
; Publication No. US20030022821A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 22, Application US/09798869
Publication No. US20030022821A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 54.5%,
".hes 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
           1 CFQWXRNMRKV 11
                                                3 CYQWQWRMRKL 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CFOWXRNMRKV 11
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US-09-798-869-22
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TYPE: PRT
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US-09-798-869-7
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2; Indels
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                                                                                                                         RESULT 6

US-09-798-869-23

Sequence 23, Application US/09798869

PUDLICATION NO. US2003002281A1

GENERAL INFORMATION:
APPLICANT: JOHN SIGHED SVENDSEN
APPLICANT: GENERAL BALDUR SVENDSEN
APPLICANT: HARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT-GB99/02851
PRIOR APPLICATION NUMBER: PCT-GB99/02851
PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PSIOR APPLICATION NUMBER: PSIOR APPLICATION NUMBER: PSIOR SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 23

LENGTH: 25
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APPLICANT: (YSTEIN REKDAL
APPLICANT: ABLONG SVEEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: AJ4049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: CT/GB99/02651
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-28
SOFTWARE: FEASTEQ FOR Windows Version 4.0
SEQ ID NO 7
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Publication No. US20030022821A1
GENERAL INFORMATION:
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Best Local Similarity 63.00
-20 7; Conservative
                               CFOWXRNMRKV 11
                                                                         3 CYÓWORRMRKL 13
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; Sequence 29, Application US/09798869; Publication No. US20030022821A1. GENERAL INPORMATION: APPLICANT: JOHN SIGURD SVENDSEN
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Matches 5; Conserv
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ORGANISM: BOVINE
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JS-09-798-869-29
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US-09-798-869-30
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       Sequence 2, Application US/09888320
Fublication No. US20030013090A1
GENERAL INFORMATION:
APPLICANT: Barry III, Clifton E.
APPLICANT: Moduli, Khishmuzi
APPLICANT: Beker, Linda-Gail
APPLICANT: Be presented by The Secreteary of the
APPLICANT: Department of the United States of America
APPLICANT: Department of Health and Human Services
ITTLE OF INVENTION: Methods of Diagnosing Multidrug Resistant Tuberculosis
FILE REPRENCE: 012820-4413100U3
CURRENT APPLICATION NUMBER: US/09/888,320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          55.2%; Score 37; DB 9; Length 489; 54.5%; Pred. No. 36; tive 2; Mismatches 3; Indels
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APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
TILE REFERENCE: A34049-PCT-USA-A
CURRENT FILING DATE: 2001-02-27
PRIOR APPLICATION NUMBER: US/09/798,869
PRIOR APPLICATION NUMBER: PCT/GR89/02851
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1998-08-38
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/214,187 BYOR FILING DATE: 2000-06-26 NUMBER OF SEQ ID NOS: 16 SOFTWARE: Patentin Ver. 2.1
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APPLICANT: JOHN SIGNED SVENDSEN; APPLICANT: (YSTEIN REKDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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Best Local Similarity 54.5%,
"whos 6; Conservative
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Matches 6; Conserv
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LENGTH: 15
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APPLICANT: (YSTEIN REKOAL)
APPLICANT: (YSTEIN REKOAL)
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BIOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT APPLICATION NUMBER: PCT/G899/02851
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1999-08-31
PRIOR PILING DATE: 1998-08-28
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PREUSED for Windows Version 4.0
SSOFTWARE: PREUSED for Windows Version 4.0
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APPLICANT: (YSTEIN RENDAL
APPLICANT: BALDUR SVEINBJ (RNSSON
APPLICANT: LARS VORLAND
TITLE OF INVENTION: BLOACTIVE PEPTIDES
FILE REFERENCE: A34049-PCT-USA-A
CURRENT APPLICATION NUMBER: US/09/798,869
CURRENT FILING DATE: 1999-08-31
PRIOR RILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-31
PRIOR FILING DATE: 1999-08-38
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PASESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 15
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3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 30, Application US/09798869
Publication No. US2030022821A1
GENERAL INFORMATION:
APPLICANT: JOHN SIGURD SVENDSEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5; Conservative
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Matches 5; Conserv
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50.7%; Score 34; DB 9; Length 86; 45.5%; Pred. No. 23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: Up 9/1738,626
PRIOR PLOR APPLICATION NUMBER: UP 99/377484
PRIOR FLING DATE: 1999-12-16
PRIOR PLING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: UP 00/159162
PRIOR APPLICATION NUMBER: UP 00/280989
PRIOR PLING DATE: 2000-04-07
PRIOR PLING DATE: 2000-08-03
NUMBER OF FILE DE NOS: 7059
SOFTWARE: PATENTIN VET. 3.0
FROM IN NO 5715
FROM DEATH OF THE NET. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: February 21, 2003, 08:11:55 Job time : 6.88372 secs
                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 249-125
CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-5715
                                                                                      MIZOGUCHI, HIROSHI
ANDO, SEIKO
                                                                                                                                                 HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                          NAKAGAWA, SATOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 45.5
Matches 5; Conservative
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APPLICANT:
APPLICANT:
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APPLICANT: Penn, Sharron S.
APPLICANT: Rank, David R.
APPLICANT: Hantel, David R.
APPLICANT: Chen, Wenshing
ITILE OF INVENTION: HUANG GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ITILE OF INVENTION: HUANG GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUANG GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL SOUTH OF TITLE OF INVENTION WINDER: US 60/180,312
READ PRILOMION NUMBER: US 60/180,312
READ PRILOMION NUMBER: US 60/207,456
READ PRILOM DATE: 2000-02-04
READ PRILOM PROBES: US 60/207,456
READ PRILOM NUMBER: PCT/US01/00666
READ PRILOM DATE: 2000-09-27
READ PRILOM DATE: 2001-01-30
READ PRILOM NUMBER: PCT/US01/00667
READ PRILOM NUMBER: PCT/US01/00667
READ PRILOM NUMBER: PCT/US01/00667
READ PRILOM NUMBER: PCT/US01/00669
READ PRILOM NUMBER: PCT/US01/00669
READ PRILOM NUMBER: PCT/US01/00669
READ PRILOM DATE: 2001-01-30
READ PRILOM DATE: 2001-01-30
READ PRILOM DATE: 2001-01-30
READ PRILOM NUMBER: PCT/US01/00665
READ PRILOM DATE: 2001-01-30
READ PRINCE DATE: 2001-01-30
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OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN HEA4, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
US-09-864-761-47985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 47985
LENGTH: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRICR AFFLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR APPLICATION NUMBER: ACT/US01/00670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-01-50
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR PLING DATE: 2000-06-30
PRIOR PILING DATE: 2001-01-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 5; Conserva
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; Sequence 5715, Application US/09738626
; Publication No. US20020197605A1
; GENERAL INFORMATION:

US-09-738-626-5715

RESULT 15

16 CFÓWRR 21

0

Gaps

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on:

February 21, 2003, 07:48:01; Search time 10.6047 Seconds (without alignments) 108.784 Million cell updates/sec

US-09-743-107B-88 1 CFQWXRNMRKVR 12 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

73:* PIR Database :

1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

lactotransferrin p lactoferrin - goat lactoferrin - shee hypothetical prote lactoferrin precur En/Spm-like transp prote probable pyridoxam hypothetical prote hypothetical prote apolipoprotein B-1 probable monooxyge F1511.22 [imported hypothetical prote protein - myx hypothetical prote outer capsid prote hypothetical sh3-c probable proteinas histoc histidyl-tRNA synt carcinoembryonic a 26S proteasome SU pyridoxamine 5'-ph hypothetical prote pyridoxamine 5'-ph dynein beta heavy protein F21H11.2 hypothetical MHC class I Description MAP1 S52107 AB0858 T22597 A28438 A84471 T24218 T08030 B60950 A45687 D88450 S67085 AB2154 E90094 H97451 Query Match Length DB Score . 02 Result

hypothetical prote RNA la protein - b	phytochrome C - so	pyruvate carboxyla pyruvate carboxyla	probable helicase	trichohyalin like	resistance protein	protein UNC-89 - C	vif protein - simi	hypothetical prote	ardinyltransferase	Signal mentidase I	33 3K hymorhatical	CONSENTED DIMOTHER	hypothetical prote
20 BB	98	11	78	31	63	57	89	36	01	15	03	34	11
T2882(P1BVB	T14803	AE29	T41378	B8543	T30563	T297	8079	D89836	AI3401	E87515	G86403	C8223	T3321
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30	3 8	34	9 1	1 Q	, c	י סכ דו	o.	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

TFHUL lactotranaferrin premireor (validated) - human
NyAlternate names: lactoferrin
C;Species: Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence revision 21-Nov-1997 #text change ns-ned cond
C; Accession: G01394; S11228; A45401; S10324; S15853; S07150; S07150; S07150
R;Cho, Y.
submitted to the EMBL Data Library, March 1994
A;Reference number: G06820
A;Accession: G01394
A; Status: preliminary: translated from GB/EMBI, / ppg.
A; Molecule type: mRNA
A; Residues: 1-711 < CHO>

A, Cross-references: EMBL:U07643; NID:g467236; PIDN:AAB60324.1; PID:g467237 R,Rey, M.W.; Woloshuk, S.L.; deBoer, H.A.; Pieper, F.R. Nucleic Acids Res. 18, 5288, 1990
A,Title: Complete nucleotide sequence of human mammary gland lactoferrin. A, Reference number: S11228; MUID:90384839; PMID:2402455

A; Accession: S11228

A Molecule type: mRNA
A;Residues: 1-148, T'.150-422, C', 424-711 <REY>
A;Crost-references: EMBL:X53961; NID:924415; PIDN:CAA37914.1; PID:934416
A;Crost-references: EMBL:X53961; Nalmer, D.; Panella, T.
Mol. Endocrinol. 6, 1969-1981, 1992
A;Tille: Differential molecular mechanism of the estrogen action that regulates lactofern A;Reference number: A45401; MUID:93125571; PMID:1480183

A;Molecule Lype: DNA
A;Residues: 1-15 <TEN>
A;Residues: 1-15 <TEN>
A;Residues: 1-15 <TEN>
A;Cross-references: GB:52659; NID:g263311; PIDN:AAB24877.1; PID:g263312
A;Experimental source: placenta
A;Note: sequence extracted from NCBI backbone (NCBIP:122202)
B;Powell: M.J; Ogden, J.B.
Nucleic Acids Res. 18, 4013, 1990
A;Title: Nucleotide sequence of human lactoferrin cDNA.
A;Reference number: S10324; MUID:90326549; PMID:2374734

A; Accession: S10324

A.Molecule type: mRNA
A.Residues: 3-711 <POW>
A.Residues: 3-711 <POW>
A.Residues: 3-711 <POW>
A.Cross-references: BMB.:X52941; NID:g34411; PIDN:CAA37116.1; PID:g34412
R.Stowell, K.M.; Rado, T.A.; Funk, W.D.; Tweedie, J.W.
Biochem. J. 276, 349-355, 1991
A.Title: Expression of cloned human lactoferrin in baby-hamster kidney cells.
A.Reference number: S15853; MUID:91264786; PMID:2049066

A)Status: nucleic acid sequence not shown; not compared with conceptual translation A,Molecule type: mRNA A,Residues: 20-31 <8T1> A,Accession: S20841 A,Accession: S20841 A,Molecule type: protein A,Residues: 20-28, X', 30-31 <\$T2>

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Gaps

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Appointerical protein STY3070 [imported] - Salmonella enterica subsp. enterica serovar Typhi C.Species: O9-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001 C.Accession: AB0858 R.Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T. T.; Connerton, P.; Cronin, A.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P. Nature 413, 848-852, 2001 A.Authors: Park C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A.Authors: Asserved enome sequence of a multiple drug resistant Salmonella enterica seroval, A.Accession: AB0858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: S52107
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
R;Qian, Z.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
R;Qian, E.Y.; Jolles, P.; Migliore-Samour, D.; Fiat, A.M.
A;Title: Isolation and characterization of sheep lactoferrin, an inhibitor of platelet A;Reference number: S52107; MUID:95127729; PMID:7827104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: GB: AL513382; PIDN: CAD06049.1; PID: 916504016; GSPDB: GN00176
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 14-Jul-1995 #sequence_revision 05-Dec-1997 #text_change 05-Dec-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein F53H4.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000
                                                             Length 708;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67.2%; Score 45; DB 2; Length 33; 54.5%; Pred. No. 0.12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Modecule type: protein
A;Residues: 1-33 <QIA>
C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2;
Pred. No. 9.1;
0; Mismatches
                                                          Score 48; DB 2;
Pred. No. 0.65;
                                                                                                                           Mismatches
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                                                          71.6%; Sco
63.6%; Pre
tive 2;
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58.3%;
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                                                                                                                           Conservative
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                                                Query Match
Best Local Similarity
                                                                                                                                                                                  1 CFQWXRNMRKV 11
                                                                                                                                                                                                                                                    38 CYQWQRRMRKL 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CFOWXRNMRKV 11
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A; Residues: 1-511 < PAR>
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                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 436-487, /A', 489-711 < RAD>
A; Cross-references: EMBL:M18642; NID:9186815; PIDN:AAA86665.1; PID:9386855
R; Panella, T.J.; Liu, Y.; Huang, A.T.; Teng, C.T.
Cancer Res. 51, 3037-3043, 1991
A; Title: Polymorphism and altered methylation of the lactoferrin gene in normal leukocyt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: protein
A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A; Residues: 20-140,142-169,171-203,'L',205,'K',207-208,'K',210-385,'Q',387-391,'W',393-4
A; Note: this is the final paper in a series
R; Houen, G.; Hoegdall, B.V.; Barkholt, V.; Norskov, L.
Bur. J. Blochem. 241, 303-308, 1996
A; Title: Lactoferrin: similarity to diamine oxidase and purification by aminohexyl affin
A; Reference number: S74119; MUID:97054624; PMID:8898921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R,Metz-Boutigue, M.H.; Jolles, J.; Mazurier, J.; Schoentgen, F.; Legrand, D.; Spik, G.; Eur. J. Biochem. 145, 659-666, 1984
A;Title: Human lactotransferrin: amino acid sequence and structural comparisons with oth A;Reference number: A31000; MUID:85076667; PMID:6510420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-May-1999
C;Accession: JC2233
R;Le Provost, F.; Nocart, M.; Guerin, G.; Martin, P.
Biochem. Biophys. Res. Commun. 203, 1324-1332, 1994
A;Title: Characterization of the goat lactoferrin cDNA: assignment of the relevant locus A;Reference number: JC2323; MUID:94380047; PMID:8093048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;21-356/Domain: transferrin repeat homology <TRH1>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;360-699/Domain: transferrin repeat homology <TRH2>
F;29-65,39-56,135-218,177-193,190-201,251-266,503-697,595-609/Disulfide bonds: #status e
F;157,498/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;368-400,378-391,425-706,447-669,479-554,513-527,524-537,647-652/Disulfide bonds: #stat
R;Rado, T.A.; Wei, X.; Benz Jr., E.J.
Blood 70, 989-993, 1987
A;Title: Isolation of lactoferrin cDNA from a human myeloid library and expression of A;Reference number: S07160; MUID:88001031; PMID:3477300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A/Accession: JC2223
A,Molecule type: mRNA
A/Residues: 1-708 - LEEP-
C,Superfamily: transferrin; transferrin repeat homology
C,Keywords: duplication; glycoprotein
F;359-696/Domain: transferrin repeat homology <TRH2>
F;252,300,387,495,564/Binding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 0.0005;
1; Indels
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A:Map Position: 3421-3423
C;Superfamily: transferrin; transferrin repeat homology
C;Reywords: duplican; glycoprotein; iron binding; milk
F;1-19/Domain: signal sequence #status predicted <SIG>F;20-711/Product: lactotransferrin #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A61169; MUID:91235214; PMID:16744448
A; Accession: A61169
                                                                                                                                                                                                                                                                                                                                                                                                                                A, Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A;Residues: 'G',23-24,'R',26-27,'XX',30-32 <HOU>
A;Experimental source: neutrophil granulocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Experimental source: normal breast tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 3-701, 'SWKPVN' <PAN>
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Best Local Similarity 91.77
Trahes 11; Conservative
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                                                                                                                                      A; Accession: S07160
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C;Genetics:

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Gaps

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C; Accession: T22597

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Gaps

Query Match

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C)Species: Chlamydomonas reinhardtii
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 02-Feb-2001
C;Date: 21-May-1999 #sequence R;Mitchell, D.R.; Brown, K.S.
J. Cell Sci. 107, 635-644, 1994
A;Title: Sequence analysis of the Chlamydomonas alpha and beta dynein heavy chain genes.
A;Reference number: 216302; MUID:94274778; PMID:8006077
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2;34/4; 3, 3666/3; 3882/3; 4240/3
C;Superfamily: dynein heavy chain, ciliary
C;Keywords: nucleotide binding; P-loop
F;1919-1926/Region: nucleotide-binding motif A (P-loop)
                     A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: EMBL: Z35602; PIDN: CAA84671.1; GSPDB: GN00021; CESP:R13G10.2
                                                                        A;Accession: A84471
A;Status: prefilminary
A;Molecule type: DA
A;Residues: 1-531 <STO>
A;Ccoss-references: GB:AE002093; NID:g4586022; PIDN:AAD25641.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein R13G10.2 - Caenorhabditis elegans
C;Species: caenorhabditis elegans
C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct.1999
C;Accession: T24218
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A;Experimental source: strain 21gr
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                                                                                                                                                                                                                                                                                                                                              56.7%; Score 38; DB 2; Length 531; 75.0%; Pred. No. 34;
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A;Accession: T24218
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 38; DB 2;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dynein beta heavy chain - Chlamydomonas reinhardtii
                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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submitted to the EMBL Data Library, August 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
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A;Map position: 3
A;Introns: 64/3; 194/1; 404/3
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A; Residues: 1-4568 <MIT>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        501 OWFRINKK 508
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A;Gene: At2g05650
A;Map position: 2
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C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
R;Pentecost, B.T.; Teng, CT.
J. Biol. Chem. 262, 10134-10139, 1987
A;Title: Lactotransferrin is the major estrogen inducible protein of mouse uterine secre
A;Reference number: A32596; MUID:87280033; PMID:3611056
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: O2-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: A84471
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. Nature 402, 761-768, 1999
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                                                                                                             A Status: preliminary; translated from GB/EMBL/DDBJ
A;Nolecule type: DDA
A;Residues: 1-275 -WIL.>
A;Cross-references: EMBL:Z81089; PIDN:CAB03137.1; GSPDB:GN00028; CESP:F53H4.4
A;Experimental source: clone F53H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R.Liu, Y.; Teng, C.T.
J. Biol. Chem. 266, 21880-21885, 1991
A;Title: Characterization of estrogen-responsive mouse lactoferrin promoter.
A;Reference number: A41205; MUID:92042099; PMID:1939212
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A,Residues: 1-15 <LIU>
A,Residues: 1-15 <LIU>
A,Residues: 1-15 <LIU>
A,Cross-references: GB:M/4478
C,Superfamily: transferrin; transferrin; transferrin; transferrin; transferrin; transferrin; E/20-107/Product: lactotransferrin #status predicted <SIG>F:1-19/Domain: signal sequence #status predicted <MAT>F:20-707/Product: lactotransferrin #status predicted <MAT>F:28-695/Domain: transferrin repeat homology <TRH2>F:494/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Introns: 67/1; 153/1
C;Superfamily: Caenorhabditis elegans hypothetical protein F53H4.4
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Pred. No. 12;
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R;Dobson, R. submitted to the EMBL Data Library, October 1996 A;Reference number: 219587 A;Referession: T22597
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N,Alternate names: lactotransferrin
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A,Residues: 3-707 <PEN>
A,Cross-references: EMBL:J03298
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Matches 7; Conservative
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Matches 6; Conserv
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A;Gene: CESP:F53H4.4
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